STIC-Biotech/ChemLib

156047

From:

Swope, Sheridan

Sent:

Thursday, June 09, 2005 5:56 PM

To:

STIC-Biotech/ChemLib

Subject:

10/649,273

For 10/649,273, pls search and interference search:

SID 2:

full-length against the NT data bases 148-414 against the NT data bases 176-414 against the NT data bases

Sheridan Swope, Ph.D.
Patent Examiner, AU 1652
Recombinant Enzymes
571-272-0943 (voice)
E02B71 Remsen Bld (Office)
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Row Schulwitz

STAFF USE ONLY
Searcher:
Searcher Phone: 2-
Date Searcher Picked/up:
Date Searcher Picked up: Date Completed:
Searcher Prep/Rev. Time:
Online Time:

Type of Search

NA#:____ AA#:___
Interference:___ SPDI:__
S/L:__ Oligomer:___
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Inventor:__ Litigation:__

Vendors and cost where applicable STN:

DIALOG:
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SEQUENCE SYSTEM:
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-Q-/cgn2 1/USPTO spool_p/US10649273/runat_15062005_111416_6030/app_query.fasta_1.1429
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-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DCCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN0 -MAXLEN=2000000000
-USER-US10649273 @CGN 1 _7742 @runat 15062005_111416_6030 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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ALIGNMENTS

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ACCESSION VERSION KEYWORDS SOURCE ORGANISM RESULT 1 BC011904 REFERENCE DEFINITION Snoo AUTHORS Strausberg, R. L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Strausberg, R. L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, P.S., Wagner, L., Shemmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Altschul, S.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, P.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Stapleton, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Halc, S., Gazcia, A.M., Gay, L.J., Richards, S.,
Willalon, D.K., Muzny, D.M., Sodergren, B.J., Lu, X., Glabs, R.A.,
Pahen, T., Walton, R. Kertenan, M. Madan, A. Dodaffiches Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1998) BC011904 1908 bp mRNA linear Homo sapiens O-sialoglycoprotein endopeptidase-like clone MGC:20293 IMAGE:4121450), complete cds. Fahey, J., Helton, B., F Sanchez, A., Whiting, M. Homo sapiens Homo sapiens (human) BC011904.2 GI:40225818 Blakesley,R.W., Ketteman,M., Madan,A., Rodrigues,S., M., Madan,A., Young,A.C., Shevchenko,Y., sley,R.W., Touchman,J.W., Green,E.D., PRI 23-DEC-2003 mRNA (cDNA

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Contact: nisc_mgc@nhgri.nih.gov
Akhter,N., Ayele,K., Beckstrom_Sternberg,S.M., Benjamin,B.,
BlakesLey,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,O.L., Masiello,C., Masierins,B.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
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CDNA Library Arrayed by: The I.M.A.G.E. Consortiu
DNA Sequencing by: National Institutes of Health
Sequencing Center (NISC),
Gaithersburg, Maryland;
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on Dec 19, 2003 this sequence
Contact: MGC help desk
Email: cgapbs r@mail.nih.gov
Tissue Procurement: ATCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 28 Row: i Column: 22.
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Submitted (30-JUL-2001) National Institutes of Health, Mammalian Gene Collection (MCC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg, R.
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                                                        ThrHisArgAlaIleLeuPheCysLysGlnArgAspLeuLeuProGlnAsnAsnAlaVal 320
                                                                                                                                       SerAlaAlaAspIleAlaAlaThrValGlnHisThrMetAlaCysHisLeuValLysArg
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Sequence 1 :
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Chen, J., Feder, J.N., Nelson, T.C., Krystek, S.R. and Polynucleotides encoding a novel metalloprotease, Patent: US 6642041-A 1 04-NOV-2003;
Location/Qualifiers
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Chen,J., Feder,J.N.,
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Sequence 21
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 Nelson, T.C.,
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GlyGluAlaSerIleLysValProGlnLeuLysMetGluIle 414
                                              IleMetIleAlaTrpAsnGlyIleGluArgLeuArgAlaGlyLeuGlyIleLeuHisAsp
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Krystek, S.R.

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Location/Qualifiers
                                                                                                                 GlyGlyLysAlaIleGluHisLeuAlaLysGlnGlyAsnArgPheHisPheAspIleLys
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GATAAAATAATAATGAAAAAGGAAAAAGGGAAGGTATATTTCTAATTAGTAAAGTTGAA
              AspLysIleIleMetLysLysGluLysGluGluGlyIle------
                                                 CCTCCCTTGCATCATGCTAAAAATTGTGATTTTTCTTTTACTGGACTTCAACACGTTACT
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Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniat
Mammalia; Eutheria; Primates; Catarri
                                                                                                                                                                                                                                                                                                     Submitted (27-OCT-2000) Chen J.M., Laboratory, The Babraham Institute,
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	GATAAAATAATGAAAAAGGAAAAAGGGAAGGTATATTTCTAATTAGTAAAGTTGAA 863	b 804	문
	AspLysIleIleMetLysLysGluLysGluGluGluTle	у 261	5
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	GlyGlyLysAlaIleGluHisLeuAlaLysGlnGlyAsnArgPheHisPheAspIleLys 240	y 221 b 684	음 ઇ
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	ProPheIleProIleHisHisMetGluAlaHisAlaLeuThrIleArgLeuThrAsnLys 160	y 141	ð
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		26	문 .
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	TIGGGAGAAGCAATACATTCCCAAACTGAAGTTCATTTAAAAACAGGTGGGATTGTTCCT 263	. 2	밁
	LeuGlyGluAlaIleHisSerGlnThrGluValHisLeuLysThrGlyGlyIleValPro 80	y 61	ર્
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	GluPheLeuArgSerPheAsnPheHisProGlyThrLeuPheLeuHisLysIleValLeu 40	y 21	ð
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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GlyGluAlaSerIleLysValProGlnLeuLysMetGluIle 414
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                                                                                                                   IleMetIleAlaTrpAsnGlyIleGluArgLeuArgAlaGlyLeuGlyIleLeuHisAsp
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AlaSerGlyValSerProSerAspLeuSerAlaIleAlaThrThrIleLysProGlyLeu 120

CCAGCAGCTCAACAGCTTCACAGAGAAAATATTCAACGAATAGTACAAGAAGCTCTTTCT ProAlaAlaGlnGlnLeuHisArgGluAsnIleGlnArgIleValGlnGluAlaLeuSer 100 TTGGGAGAAGCAATACATTCCCCAAACTGAAGTTCATTTAAAAACAGGTGGGATTGTTCCT

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LeuGlyGluAlaIleHisSerGlnThrGluValHisLeuLysThrGlyGlyIleValPro

GlyIleGluThrSerCysAspAspThrAlaAlaAlaValValAspGluThrGlyAsnVal

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GAATTTTTAAGAAGTTTTAATTTTCATCCTGGAACACTATTTCTTCATAAAATAGTATTG

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               1 MetLeuIleLeuThrLysThrAlaGlyValPhePheLysProSerLysArgLysValTyr
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38650, 28472, 5495, 65507, 81588 and 14354
of human proteins and uses thereof
Patent: WO 02074960-A 4 26-SEP-2002;
Millennium Pharmaceuticals, Inc. (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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kgeptlyllisgchcllalvogvsdflllgksldiapcdmldkvarrlslikhpecst
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ralbiltnatoctllcbprlctdngimiamngiblragigihdibgirtrbekcpl
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Eukaryota;
Mammalia; E
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                                                                                                                                                                                                                                                                                                             LeuValAlaSerGlyGlyValAlaSerAsnPheTyrIleArgArgAlaLeuGluIleLeu
                                                                                                                                                                                                                                                                                                                                           ThrHisArgAlaIleLeuPheCysLysGlnArgAspLeuLeuProGlnAsnAsnAlaVal
                                                                                                                                                                                                                                                                                                                                                                                               SerAlaAlaAspIleAlaAlaThrValGlnHisThrMetAlaCysHisLeuValLysArg
                                                                                                                                                                                                                                                                                                                                                                                                                                       AspLysIleIleMetLysLysGluLysGluGluGlyIleGluLysGlyGlnIleLeuSer
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          Chordata;
Primates;
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         Craniata; Vertebrata; Catarrhini; Hominidae;
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Patent: EP 1293569-A 400
Helix Research Institute
Biotechnology (JP)
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          GlyGlyLysAlaIleGluHisLeuAlaLysGlnGlyAsnArgPheHisPheAsplieLys
                                                                                                                                                                                                                                                                                                                                            LeuGlyGluAlaIleHisSerGlnThrGluValHisLeuLysThrGlyGlyIleValPro
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                                                 LeuAspLysValAlaArgArgLeuSerLeuIleLysHisProGluCysSerThrMetSer
                                                                                          GlnGlyValSerAspPheLeuLeuLeuGlyLysSerLeuAspIleAlaProGlyAspMet
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Ota,T., Suzuki,Y., Nishikawa,T., Otsuki,T., Sugiyama,T., Irie,R., Wakamatsu,A., Hayashi,K., Sato,H., Nagai,K., Kimura,K., Makita,H., Sekine,M., Obayashi,M., Nishi,T., Shibahara,T., Tanaka,T., Ishii,S., Yamamoto,J., Saito,K., Kawai,Y., Isono,Y., Nakamura,Y., Nagahari,K., Yawamoto,J., Saito,K., Kawai,Y., Isono,Y., Nakamura,Y., Nagahari,K., Yawada,T., Iwayanagi,T., Wagatsuma,M., Shifatori,A., Sudo,H., Hosoiri,T., Kaku,Y., Kodaira,H., Kondo,H., Sugawara,M., Takahashi,M., Kanda,K., Yokoi,T., Furuya,T., Kikkawa,E., Omura,Y., Abe,K., Kamihara,K., Katsuta,N., Sato,K., Kikkawa,K., Pujimori,K., Tanai,H., Kimata,M., Watanabe,M., Hiraoka,S., Chiba,Y., Ishida,S., Ono,Y., Takiguchi,S., Watanabe,S., Yosida,M., Hotuta,T., Kusano,J., Kanehori,K., Takahashi-Fuji,A., Hara,H., Tanasae,T., Nomura,Y., Togiya,S., Komai,F., Hara,R., Takeuchi,K., Arita,M., Imose,N., Musashino,K., Yuuki,H., Oshima,A., Sasoki,N., Actsuka,S., Yosikawa,Y., Matsunawa,H., Ichihara,T., Shiohata,N., Sano,S., Moriya,S., Momiyama,H., Satoh,N., Takami,S., Terashima,Y., Suzuki,O., Nakagawa,S., Senoh,A., Mizoguchi,H., Sugiyama,A., Takemoto,M., Kawakami,B., Yamazaki,M., Watanabe,K., Kumagai,A., Itakura,S., Fukuzumi,Y., Fujimori,Y., Kawahami,S., Fukuzumi,Y., Fujimori,Y., Kawakami,T., Oho,T., Yamada,K., Pujii,Y., Ookamoto,S., Okitani,R., Kawakami,T., Kobatake,N., Inagaki,H., Ikema,Y., Okamoto,S., Okitani,R., Kawakami,T., Kawakami,T., Shigeta,K., Senba,T., Matsumura,K.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (B-mail:genomics@hri.co.jp, Tel:81-438-52-3986) REDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research histitute (HRI) (supported by Japan Key Technology Center etc.); 5'-& 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and
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Isogai, T., Otsuki, T. and Sugiyama, T.
Direct Submission
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GVSPSDLSAIATTIKPGLALSLGVGLSFSLQLVGQLKKPFIPIHHMEAHALTIRLTNK
VEFPFLVLLISGGHCLLALVQGVSDFLLLGKSLDIAPGDMLDKVARRLPLIKHPECST
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QILSSAADIAATVQHTMACHLVKRTHRAILFCKQRDLLFQNNAVLVASGGVASNFCIR
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/db_xref="GI:16550167"
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/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       translation="MLILTKTAGVFFKPSKRKVYEFLRSFNFHPGTLFLHKIVLGIET
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tissue_type="brain"
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                                                                                                                       ThrHisArgAlaIleLeuPheCysLysGlnArgAspLeuLeuProGlnAsnAsnAlaVal
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                                                          CTGGTTGCATCTGGTGGTGTCGCAAGTAACTTCTGTATCCGCAGAGCTCTGGAAATTTTA
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Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
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Schnerch, A., Schein, J.E., Jones, S.J., and Marza, M.A.,
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1472
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Mammalia; Eutheria; Rodentia;
1 (bases 1 to 1844)
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BC058172
Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLATE at: http://image.llnl.gov Series: IRAK Plate: 123 Row: d Column: 22
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 2131246
                                                                                                                                                                                                                              Web Bite: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov/
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
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McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA Sequencing by: National Institutes of Health Sequencing Center (NISC), Gaithersburg, Maryland;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
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Contact: MGC help desk
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   CCGTTCATCCCGATTCATCACATGGAGGCTCACGCACTGACTATTAGGCTCACCAATAAA
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possible chaperone activity [Posttranslational
modification, protein turnover, chaperones]"
/db_xref="CDD:COG0533"
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GIDISREVAEAAIKVPRLKWAL"
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/tissue_type="Mammary tumor metastatized to lung.
arose spontaneously from a senescent normal mammar
(clonal) outgrowth infected with the virus MMTV."
/clone lib="NCI CGAP Lu29"
/lab_host="DH10B"
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MSGGKA I EHLAKDGNR FHFT I NPPMQNAKNCDFS FTGLQH I TDKL I THKEKEEG I EKG
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/strain="CZECH II"
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Sequence 17
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Tang,Y.T., Zhou,P., Goodrich,R., Liu,C., Asundi,V., Zhang,J., Zhao,Q.A., Yang,Y., Xue,A.J., Wehrman,T., Wang,D. and Drmanac,R.T.
                                         Nucleic acids and polypeptides
Patent: US 6743619-A 177 01-JUN-2004;
Location/Qualifiers
                                                                                                                                               Unclassified.
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GlyLeuGlyIleLeuHisAspIleGluGlyIleArgTyrGluProLysCysProLeuGly
                                     ArgLeuCysThrAsnAsnGlyIleMetIleAlaTrnAsnGlyIleGluArgLeuArgAla
                                                                                         ArgArgAlaLeuGluIleLeuThrAsnAlaThrGlnCysThrLeuLeuCysProProPro
                                                                                                                                            LeuProGlnAsnAsnAlaValLeuValAlaSerGlyGlyValAlaSerAsnPheTyrIle
                                                                                                                                                                                               AlaCysHisLeuValLysArgThrHisArgAlaIleLeuPheCysLysGlnArgAspLeu
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Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullahy, S.J., Bonaldo, M.F., Casavant, T.L.,

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

McKernan, K.J., Malek, J.A., Gounaratne, P.H., Richards, S.,

McKernan, K.J., Malek, J.A., Grunaratne, P.H., Richards, S.,

McKernan, K.J., Malek, J.A., Malek, J.A., McKewan, P.J.,

McKernan, K.J., Malek, J.A., McKewan, P.J., McKewan, P.J.,

McKernan, K.J., Malek, J.A., McKewan, P.J., McKewan, P.J.,

McKernan, K.J., Malek, J.A., Malek, J.A., McKewan, P.J.,

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McKernan, K.J., Malek, J.A., McKewan, P.J., McKewan, P.J.,

McKernan, K.J., Malek, J.A., Malek, J., McKewan, P.J.,

McKernan, K.J., Malek, J.A., McKewan, 
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                      Clone distribution: MGC clone distribution information can be for through the I.M.A.G.B. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 162 Row: f Column: 6
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (02-AUG-2004) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                CDNA Library Preparation: Express Genomics cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Sequencing Group at the Stanford Human Center, Stanford University School of Medicine, Stanford,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Howard J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 (bases 1 to 1546)
Director MGC Project.
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Location/Qualifiers
                                                                                                                                                                                                                                                                        http://www-shgc.stanford.edu
(Dickson, Mark) mcd@paxil.stanford.edu
M., Schmutz, J., Grimwood, J., Rodriquez,
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Rodentia;
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                                                                                                                                                                                          AlaLeuSerLeuGlyValGlyLeuSerPheSerLeuGlnLeuValGlyGlnLeuLysLys
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/lab_host="DH10B"
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/db_xref="taxon:10116"
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AR428809
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VERSION
                                                                                    Percent Similarity:
Best Local Similarity:
Query Match:
                                   US-10-649-273-2 (1-414)
                                                                                                                                                            Pred. No.:
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Sequence 23 from patent
AR428809
AR428809.1 GI:40188595
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Chen, J. Feder, J. N., Nelson, T. C., Krystek, S.R. and Duclos, F. Polynucleotides encoding a novel metalloprotease, MP-1
Patent: US 6642041-A 23 04-NOV-2003;
                                                                                                                                                                                                                                                                                                                                                                                       Unknown
                                                                                                                                                                                                                                                                                                                                                                     Unclassified.
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MetGluAlaHisAlaLeuThrIleArgLeuThrAsnLysValGluPheProPheLeuVal 167
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                                                                                                                                                                                                                            mol_type="genomic"
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                                                                       3.95e-108
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Cambridgeshire gallus

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REFERENCE
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Boardman, P.E., Bonfield, J.K., Brown, W.R.A., Carder, C., Chalk, S. Croning, M.D.R., Davies, R.M., Francis, M.D., Grafham, D.V., Hubbard, S.J., Humphray, S.J., Hunt, P.J., Maddison, M., McLaren, S. Niblett, D., Overton, I.M., Rogers, J., Scott, C.E., Taylor, R.G., Tickle, C. and Wilson, S.A.
                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
                                                                                                              Gallus gallus (chicken)
Gallus gallus
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                                                                                                                                                                                                                                                                                                        ProLysCysProLeuGlyValAspIleSerLysGluValGlyGluAlaSerIleLysVal
                                                                                                                                                                                                                                                                                                                                           ATTGAAAGACTACGTGCTGGCTTGGGCATTTTACATGACATAGAAGGCATCCGCTATGAA
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Submitted (02-PRB-2004) Sanger Institute, Hinxton, Cambr.
CB10 1SA, UK. B-mail enquiries: chickest@bms.umist.ac.uk
BBSRC/Dundee/Nottingham/Sanger/Sheffield/UMIST Gallus ga
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/clone="ChEST189i14"
/clone_lib="CSEQRBN11"
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Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
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Submitted (25-OCT-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      through the I.M.A.G.E. Consortium/LLNL at: Series: IRAK Plate: 86 Row: f Column: 12.
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                                                                                                                                                                                                              MetLeuAspLysValAlaArgArgLeuSerLeuIleLysHisProGluCysSerThrMet 219
                                                                                                                                                                                                                                                                                                         ValGlnGlyValSerAspPheLeuLeuLeuGlyLysSerLeuAspIleAlaProGlyAsp
SerGlyGlyLysAlaIleGluHisLeuAlaLysGlnGlyAsnArgPheHisPheAspIle
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                                                                                            <u>AGTGGTGGAAAAGCTATAGAACAGTTGGCCAAAGACGGAAATAGATTCCATTTTACTATC</u>
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/clone="IMAGE:5053559"
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/clone_Tib="NCI_CGAP_Li9"
/lab_host="DH10B"
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/mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                   Gallus gallus (chicken)
Gallus gallus
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 1558)
Boardman, P.E., Bonfield, J.K., Brown, W.R.A., Carder, C., Chalk, S.E.,
Croning, M.D.R., Davies, R.M., Francis, M.D., Grafham, D.V.,
Hubbard, S.J., Humphray, S.J., Hunt, P.J., Maddison, M., McLaren, S.R.,
Miblett, D., Overton, I.M., Rogers, J., Scott, C.E., Taylor, R.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BX930963
                                                                                                                                                 BBSRC/Dundee/Nottingham/Sanger/Sheffield/UMIST cDNA collection from a library constructed by Elizabeth Bosch. cDNA was prepar from RNA extracted from limbs, and poly A-trimmed. BCORI-NotI cut cDNA was then ligated into vector. Vector: pBluescript II KS(+); Site_1: ECORI; Site_2: Nost: Escherichia coli DH10B.
                                                                                                                                                                                                                                                      This sequence is from the
                                                                                                                                                                                                                                                                                  Submitted (29-MAR-2004) Sanger Institute, Hinxton, Cambrid 15A, UK. E-mail enquiries: chickest@bms.umist.ac.uk On Apr 1, 2004 this sequence version replaced gi:41631491 BBSRC/Dundee/Nottingham/Sanger/Sheffield/UMIST Gallus gal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BX930963.2
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                                                                                                                      1. .1558
                                                                                                                                Location/Qualifiers
                                                                                                 organism="Gallus gallus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74
                                                                                                                                                                                                                                                                                                                               GluLysGlyGlnIleLeuSerSerAlaAlaAspIleAlaAlaThrValGlnHisThrMet
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                                  ArgLeuCysThrAspAsnGlyIleMetIleAlaTrpAsnGlyIleGluArgLeuArgAla 373
                                                                                                                                                                                                                                                        AlaCysHisLeuValLysArgThrHisArgAlaIleLeuPheCysLysGlnArgAspLeu
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   GlyLeuGlyIleLeuHisAspIleGluGlyIleArgTyrGluProLysCysProLeuGly 393
                                                                                                   AGAAAAGGACTGCAGACTCTGGCAAATGCAAACGGTTTTGCTTTTTCTGTCTCCTCCTCCA
                                                                                                                                  ArgArgAlaLeuGluIjeLeuThrAsnAlaThrGlnCysThrLeuLeuCysProProPro
                                                                                                                                                                                      LeuProGlnAsnAsnAlaValLeuValAlaSerGlyGlyValAlaSerAsnPheTyrIle
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Search Job ti	В	Ş	Db.
Search completed: June 16, 2005, 23:18:30 Job time : 4983.35 secs	1446 ATTGATATTTCCAAAAGAGTTGAAGAGGATTCCATCAGAGTGCCAAGACTAAGG 1499	394 ValAspIleSerLysGluValGlyGluAlaSerIleLysValProGlnLeuLys 411	::: 1386 GGATGTGGTATTTATACAGTACTGATGGCATCCGCTATGAACCAAAAGCTCCCCTTGGA 1445

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Command line parameters:

-MODEL-frame+ p2n.model -DEV=xlp
-Q=/Cgn2_1/USPTO_Epool_p/US10649273/runat_15062005_111415_6022/app_query.fasta_1.1429
-Q=/Cgn2_1/USPTO_Epool_p/US10649273/runat_15062005_111415_6022/app_query.fasta_1.1429
-DB=N_Geneseq_16Dec04 -QFMT=fastap -SUFFIX=p2n.rng -MINATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS-bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DCCALICN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=set -HEADSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10649273 @CGN 1 1 1063 @runat 15062005 111415 6022 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEDUT=120 -WARN_TIMEDUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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Aba93268 Human O-s
Abs76635 DNA encod
Abt23207 Human pro
Aad46856 Human gly
Aca60887 Human cDN
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ALIGNMENTS

RESULT 1

ABA93268
ID ABA93268 standard; cDNA; 2058 BP.

XX
AC ABA93268;
XX
DT 19-APR-2002 (first entry)
XX
DE Human O-sialoglycoproteinase-like protein encoding cDNA SEQ ID NO:1.
XX
KW Human; O-sialoglycoproteinase-like protein; OSGPLP; enzyme; gene; ss
XX
KW Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 110.1354
FT /*tag= a
FT /*tag= a
FT /*product= "O-sialoglycoproteinase-like protein"
XX
PN CN1318550-A.
XX
PD 24-OCT-2001.
XX
PP 19-APR-2000; 2000CN-00106834.
XY
PR 19-APR-2000; 2000CN-00106834.
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PR 19-APR-2000; 2000CN-00106834.
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PA (SHAN-) SHANGHAI SHENGYUAN GENE DEV CO LTD.

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Best Local Similarity:
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                                             GlnGlyValSerAspPheLeuLeuLeuGlyLysSerLeuAspIleAlaProGlyAspMet
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LeuAspLysValAlaArgArgLeuSerLeuIleLysHisProGluCysSerThrMetSer
                                                                                    ValGluPheProPheLeuValLeuLeuIleSerGlyGlyHisCysLeuLeuAlaLeuVal
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RESULT 2
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ABS76635
AC ABS7
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DT 11-D
DT NA
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                                                                                                                                                                                                                                                                                                                                                                                      Metalloprotease; MP-1; immune disorder; glutamate transport; cancer; motor neuron disorder; amyotrophic lateral sclerosis; ALS; diabètes; reproductive disorder; Kleinfelter; syndrome; germinal cell aplasia; genital wart; metabolic disorder; premature puberty; Kallman syndrome; Cushing's syndrome; neurodegenerative disease; Alzheimer's disease; Parkinson's disease; Huntington's disease; Tourette syndrome; sepsis;
                                                                                                                                                                                                                                                                           acquired immunodeficiency syndrome; AIDS; pulmonary disease; pneumoniemphysema; cystic fibrosis; vascular disorder; inflammatory disorder; neurological disorder; gene; ds.
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05-FEB-2001; 2001US-0266518P. 05-FEB-2002; 2002WO-US003353 WO200272751-A2

10-APR-2001; 2001US-0282814P

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CC The invention describes an isolated nucleic acid molecule (I) encoding a CC metalloprotease (MP-1). (I) is useful for preventing, treating, or CC ameliorating a medical condition, particularly an immune disorder, an CC aberrant glutamate transport or motor neuron disorder, such as CC anyotrophic lateral sclerosis (ALS), its juvenile form or an ALS-like CC condition. The compositions and methods are also useful for diagnosing, CC prognosticating, treating, ameliorating and/or treating disorders (CC associated with MP-1 activity, e.g. diabetes, cancer, reproductive CC disorders (e.g. Kleinfelter's syndrome, genital warts, or germinal cell CC aplasia), metabolic disorders (e.g. premature puberty, Kallman syndrome, CC or Cushing's syndrome), neurodegenerative diseases (Alzheimer's disease, CC parkinson's diseases, Huntington's disease or Tourette syndrome), liver CC and renal diseases and immune disorders (e.g. AIDS, rheumatoid arthritis CC fibrosis) and vascular, inflammatory and neurological disorders (e.g. CC fibrosis) and vascular, inflammatory and neurological disorders (e.g. Alzheimer's disease or Parkinson's disease). This sequence represents a CC metalloprotease MP1 polynucleotide
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                                                                                                                                                                             GlyGluAlaSerIleLysValProGlnLeuLysMetGluIle 414
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autoimmune; inflammatory disease; neurological disorder;

(1-2572)

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Pred.
                                                                                                  Query Match:
                          Best Local Similarity:
                                                                                                                  The invention relates to an isolated polypeptide comprising: any of 28 CC sequences of 48-1256 amino acids; a natural amino acid sequence at least CC 90% identical to the 28 amino acid sequences, 94% identical to a sequence country of 28 coids, 96% identical to a sequence of 414 amino acids, 96% identical to a sequence of 414 amino coids, or 97% identical to a sequence of 422 amino acids, all given in CC the specification; or a biologically active or immunogenic fragment of the isolated polypeptide. The polypeptides and polymucleotides are useful in diagnosing, treating and preventing diseases or conditions associated with the decreased expression of protein modification and maintenance complete (MDD), such as cell proliferative diseases (e.g. cancer, CC allergies), neurological disorders (e.g. stroke, parkinson's disease, CC epilepsy), gastrointestinal (e.g. ulcer, cirrhosis), reproductive (e.g. circhosis), developmental, vesicle trafficking disorders, and CC infections (e.g. bacterial, viral parasitic, protozoal). These are also CC useful in assessing the effects of exogenous compounds on the expression of cragments are useful in screening compounds for effectiveness as agonist CC arget polymucleotide and compounds that specifically bind to or modulate trafficity by of the polypeptides, or in altering the expression of the activity of the polypeptides. The microarray is useful in monitoring CC measuring protein.protein interactions, drug-target interactions, and CC encoding a human PMOD protein of the invention
                                      Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thangavelu K, Changavelu K, Walia NK, Mason PM, Walia NK, Muson PM, (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        diagnosing, treating and preventin with the aberrant PMOD expression,
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protein-protein interaction; drug-target interaction;
gene expression profile; human; gene; ds.
                                                                                                  Sequence
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29-AUG-2001;
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06-JUL-2001;
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2001US-0303445P.
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The present invention relates to novel 38650, 28472, 5495, 65507, 81588 or 14354 nucleic acid molecules which encode adenosine deaminane, glycoprotease or seven transmembrane domain (77M) receptor family members. Sequences of the invention are useful in diagnosing and treating cancer or aberrant cellular proliferation and/or differentiation (e.g. colon or lung cancer), immune disorders (e.g. selective IgA deficiency, rheumatoid
                                                                                                                                                                                             New 38650, 28472, 5495, 65507, 81588 or 14354 nucleic acid molecules, useful for diagnosing and treating cancer, immune, cardiovascular, hematopoietic, brain, pain, metabolic, liver or platelet disorders, a
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/product= "Human 28472 protein"
/product= "This region is specifically claimed as
6 in claim 1 of the specification"
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arthritis, diabetes, allergy), heart or cardiovascular disorders (e.g., hypertension, atherosclerosis, arrhythmias, ischaemic heart disease, myocardial infarction, thrombus) including endothelial cell disorders (e.g. psoriasis, Grave's disease), haematopoietic disorders, brain disorders (e.g. cerebral oedema, Parkinson's or Alzheimer's disease), pain and metabolic disorders (e.g. obesity), liver disorders or platelet disorders. They are also useful in screening assays, predictive medicine (e.g. diagnostic assays, prognostic assays, monitoring clinical trials and pharmacogenetics) and prophylactic and therapeutic methods. The nucleic acids may also be used in chromosome mapping, tissue typing and forensic biology and as surrogate markers. Sequences of the invention are also used in cene therapy. The present sequences of the invention are
                                                                                             used in
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Sequence 1820 ₽₽; 543 A; 365 Ç 393 <u>و</u> 518 H, 0 U; 1 Other;

Percent Similarity:
Best Local Similarity:
Query Match:

1.24e-208 2088.00 99.03% 98.31% 98.26%

Length: Matches: Mismatches: Conservative: Indels:

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                                                                             08-NOV-2000; 2000US-0246768P.
08-NOV-2000; 2000US-0246772P.
15-NOV-2000; 2000US-0249185P.
(LEIB/)
(KAPE/)
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/note= "This CDS is specifically claimed
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CC deaminase), 28472 (encoding a glycoprotease), 5495 (encoding a 7) CC deaminase), 28472 (encoding a glycoprotease), 5495 (encoding a 7) CC transmembrane receptor), 65507, 81588 or 14354 nucleic acid molecule (or ca sequence which is at least 60% identical to the six nucleic acids or ctheir open reading frames, fragments of at least 15 nucleotides, naturally occurring variants, or a DNA insert of the plasmid deposited continued the American Type Culture Collection as Accession No. not defined in the specification, which encodes the amino acid sequence). Also included care a host cell containing the nucleic acids (used to produce the proteins), the encoded proteins, an antibody that selectively binds to compound that binds to/modulates the cativity of the polypeptide. The nucleic acid molecules, polypeptides and comethods are useful for diagnosing, treating cancer, aberrant cellular compound that binds to/modulates the compound that binds to/modulates the cativity of the polypeptide. The nucleic acid molecules, polypeptides and compound that binds to/modulates the cativity of the polypeptide. The nucleic acid molecules, polypeptides and compound that binds to/modulates the cativity of the polypeptide. The nucleic acid molecules, polypeptides and comethods are useful for disgnosing, treating cancer, aberrant cellular compound that binds to/modulates, polypeptides and compound that binds to/modulates, polypeptides and comethods are useful for disgnosing, treating cancer, aberrant cellular compound that binds to/modulates, polypeptides and compound that binds to/modulates, polypeptides and comethods are useful for disgnosing, treating cancer, aberrant cellular compound that binds to/modulates and compound that binds to/modulates and compound that binds to/modulates the cativity of the polypeptide. The nucleic acid molecules, polypeptides and compound that binds to/modulates and compound that binds to/modulates and compound that binds to/modulates and compound that binds to/modulates and compound that binds to/modu
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Percent Similarity:
Best Local Similarity:
Query Match:
DB: US-10-649-273-2 (1-414) x ACA60887 (1-1820) Alignment Scores: No.: 1.24e-208 2088.00 99.03% 98.31% 98.26% Length:
Matches:
Conservative:
Mismatches:
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breast cancer; ovarian cancer; prostate cancer; colon cancer; lung cancer; immune disorder; heart disorder; cardiovascular disorder; endothelial disorder; hematopoietic disorder; blood vessel disorder; brain disorder; pain; metabolic disorder; liver disorder; diabetes; platelet disorder; carcinoma; sarcoma; leukaemia; Hodgkin's disease;
                                                                                                                                                  Cancer; aberrant cell proliferation; aberrant cell differentiation;
                                                                                                                                                                                                          cDNA encoding novel human glycoprotease 28472
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08-NOV-2000;
08-NOV-2000;
15-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                           autoimmune disorder; hypertension; atherosclerosis; heart failur myocardial infarction; ischaemic heart disease; Crohn's diseases Grave's disease; Kawasaki syndrome; Raynaud's disease; aneurysm; cerebral ischaemia; peripheral neuropathy; Alzheimer's disease; Parkinson's disease; anorexia nervosa; cachexia; glycoprotease;
                                                                                                                                                                                                                                                                                                          08-NOV-2001; 2001WO-US046724
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/product= "Glycoprotease 28472"
/note= "Specifically claimed in
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                                                                                                                                                                                                                                                                                                                                                      claim
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                                                                                                                                                                                                                                                                                                                                                                                                              gene;
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New adenosine deaminase, glycoprotease and seven transmembrane nucleic acids and polypeptides, designated 38650, 28472, 5495, 81588 and 14354, useful for treating e.g. leukemias, Hodgkin's hypertension. domain 65507, disease õ

P-PSDB;

ABG71162.

Claim 2; Fig 8A-B; 178pp; English

The invention describes isolated 38650, 28472, 5495, 65507, 81588 and CC 14354 nucleic acid molecules (I) and their encoded polypeptides (II). The CR 14354 nucleic acid molecule comprises a sequence encoding adenosine CC deaminase. The 28472 nucleic acid molecule comprises a sequence encoding CC a human glycoprotease. The 5495, 65507, 81588 and 14354 comprise CC sequences that encode a human seven transmembrane domain (7TM). The CR 28472, 5495, 65507, 81588 and 14354 comprise CC sequences are useful for diagnosing, preventing or treating a subject CC with or at risk of developing a disorder, e.g. cancer or aberrant CC cellular proliferation and/or differentiation (e.g. breast, ovarian, CC prostate, colon or lung cancer), immune disorders, heart disorders, brain disorders, pain and metabolic disorders, CC liver disorders or platelet disorders, pain and metabolic disorders, CC liver disorders or platelet disorders. These disorders include carcinoma, 1 Eukaemia, Hodgkin's disease, autoimmune disorders (asporders), atherosclerosis, heart failure, myocardial infarction, CC ischaemic heart disease, Crohn's disease, Grave's disease, Kawasaki CC syndrome, Raynaud's disease, aneurysm, cerebral ischaemia, peripheral cachexia or diabetes. This sequence encodes the novel human glycoprotease CC cachexia or diabetes. This sequence encodes the novel human glycoprotease.

Sequence 1821 ₽P; 543 Α. 365 Ç 394 ဂ 518 H. 0 U; 1 Other;

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Query
              Percent Similarity:
Best Local Similarity:
                                     80
:
         Match:
1.24e-208
2088.00
99.03%
98.31%
98.26%
Caps:
         Indels:
               Mismatches:
                      Matches:
Conservative:
1821
407
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US-10-649-273-2 (1-414)× ABS57020 (1-1821)

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| IleMetIleAlaTrpAsnGlyIleGluArgLeuArgAlaGlyLeuGlyIleLeuHisAsp
                                                             ThrAsnAlaThrGlnCysThrLeuLeuCysProProProArgLeuCysThrAspAsnGly
                                                                                                                                                                          ThrHisArgAlaIleLeuPheCysLysGlnArgAspLeuLeuProGlnAsnAsnAlaVal
                                                                                                                                                                                                                        AspLysIleIleMetLysLysGluLysGluGlyIleGluLysGlyGlnIleLeuSer
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                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
                                                                        US-10-649-273-2 (1-414) x ADA52832
                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to novel human secretory or membrane proteins (ADA54072-ADA55710) and their coding sequences (ADA52433-ADA54071). The coding sequences are useful in the gene therapy of diseases caused by abnormalities of the proteins, e.g. cancer, inflammatory diseases, osteoporosis or neurological disease.
                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New polynucleotides encoding full-length polypeptides, e.g. secretory and/or membrane proteins, useful for developing medicines for diseases which the gene is involved, or as target molecules for gene therapy.
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P-PSDB; ADA54471.
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24-JAN-2002; 2002US-0350435P.
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                                                         IleMetIleAlaTrpAsnGlyIleGluArqLeuArqAlaGlyLeuGlyIleLeuHisAsp 380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Early detection of soft tissue sarcoma comprises determining expression of a gene in a first soft tissue sample and a normal soft tissue sample and comparing the gene expression, also useful in treating soft tissue
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The invention relates to a novel method for detecting soft tissue sarcoma which comprises obtaining a first soft tissue sample from an individual and a normal soft tissue sample from the same or different individual, determining the expression of a gene in both samples and comparing the expression in the first soft tissue samples and comparing the expression in the first soft tissue samples and comparing the presence of soft tissue sarcoma. The method of the invention has cytostatic applications and may be useful for detecting soft tissue sarcoma, possibly via gene therapy or vaccine production. The nucleic acid sequences may be useful in diagnostic and screening applications. The current sequence is that of a human soft tissue sarcoma-upregulated DNA of the invention. The current sequence is not shown within the specification per se but was submitted in CD format by the inventor.

Sequence 2890 BP; 869 A; 609 Ç 611 <u>و</u> 789 H 0 U; 12 Other,

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Percent Similarity:
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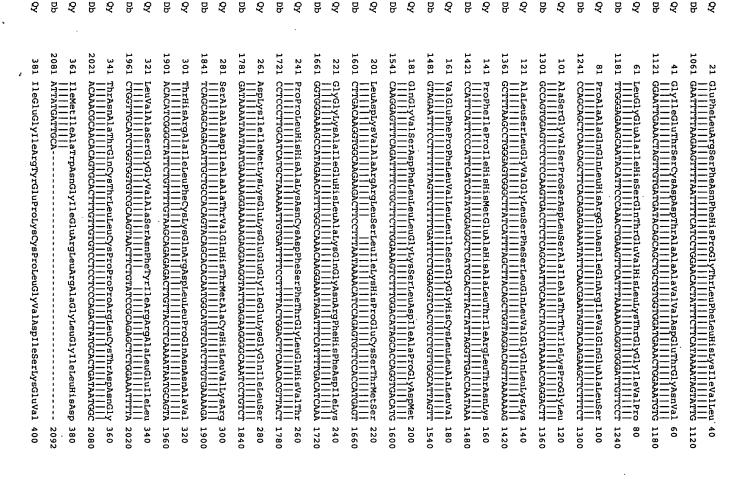
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29-JAN-2002; 2002WO-US001222

30-JAN-2001; 2001US-00774528

(GOOD/) GOODRICH × Ξ

Tang TY, Liu C, Yang Y, Zhou P, Wehrman Asundi V, T, Wang J, Zhang Wang 'n, Zhao QA, Drmanac 1 RT;

Novel polypeptide useful for treating neurodegenerative diseases, myeloid or lymphoid cell disorders, bone disorders, mechanical and traumatic disorders, coagulation disorders, and inflammatory diseases.

Claim 1; Page; 612pp; English

CC Alzheimer's disease; autolomune disease (e.g. systemic lupus (c.g. rythematosus, rheumatoid arthritis, insulin-dependent diabetes mellitus) (c.g. rythematosus, rheumatoid arthritis, insulin-dependent diabetes mellitus) (c.g. rythematosus, rheumatoid cell disorders (e.g. anaemia and thrombocytopaenia) (c.g. wounds, ulcers, burns; bone disorders (e.g. osteoporosis, vounds, ulcers, burns; bone disorders (e.g. osteoporosis, laterial) (c.g. trauma); lung or liver fibrosis; reperfusion injury in various tissues; (c.g. bacterial, viral or fungal infections; allergic conditions such as compared and inflammatory diseases (e.g. haemophilia); (c.g. ancer and tumours; and inflammatory diseases (e.g. septic shock, Crohn's (diseases, anaphylaxis). The protein may be used to inhibit the growth, (c.g. infection or function of infectious agents such as bacteria, fungi, (c.g. right) (c.g. truses, or to effect bodily characteristics, biorhythms or circadian cycles of rhythms. The protein may also have (c.g. truses) (c.g. tru This invention relates to the cDNA sequences encoding an isolated novel human polypeptide. The protein encoded by the nucleic acid of the invention is useful for treating central and peripheral nervous system diseases (e.g. peripheral neuropathy, Huntington's disease, amyotrophic lateral sclerosis); neurodegenerative diseases (e.g. Parkinson's disease

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ArgArgAlaLeuGluIleLeuThrAsnAlaThrGlnCysThrLeuLeuCysProProPro
                                                     LeuProGlnAsnAsnAlaValLeuValAlaSerGlyGlyValAlaSerAsnPheTyrIle
                                                                                             GCATGTCATCTTGTGAAAAAGAACACATCGGGCTATTCTGTTTTTGTAAGCAGAGAGACTTG
                                                                                                           AlaCysHisLeuValLysArgThrHisArgAlaIleLeuPheCysLysGlnArgAspLeu
                                                                                                                                                   GAGAAGGGGCAAATCCTGTCTTCAGCAGCAGACATTGCTGCCACAGTACAGCACACAATG
                                                                                                                                                                 GluLysGlyGlnIleLeuSerSerAlaAlaAspIleAlaAlaThrValGlnHisThrMet
                                                                                                                                                                                                        ACTGGACTTCAACACGTTACTGATAAAATAATAATGAAAAAGGAAAAAGAGGAAGGTATT
                                                                                                                                                                                                                        ThrGlyLeuGlnHisValThrAspLysIleIleMetLysLysGluLysGluGluGlyIle
                                                                                                                                                                                                                                                                            ArgPheHisPheAspIleLysProProLeuHisHisAlaLysAsnCysAspPheSerPhe
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                                                                                                                                                                                                                                                                                                                                    ProGluCysSerThrMetSerGlyGlyLysAlaIleGluHisLeuAlaLysGlnGlyAsn
                                                                                                                                                                                                                                                                                                                                                                        AspIleAlaProGlyAspMetLeuAspLysValAlaArgArgLeuSerLeuIleLysHis
                                                                                                                                                                                                                                                                                                                                                                                                                              CACTGTCTGTTGGCATTAGTTCAAGGAGTTTCAGATTTTCTGCTTCTTGGAAAGTCTTTG
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                                         TTACCTCAAAATAATGCAGTACTGGTTGCATCTGGTGGTGGCCAAGTAACTTCTATATC
                                                                                                                                                                                                                                                              AGATTTCATTTTGACATCAAACCTCCCTTGCATCATGCTAAAAATTGTGATTTTTCTTTT
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The present invention describes a non-human transgenic animal (I) C comprising a disruption in a protease target gene (PG) selected from CC calcium activated neutral protease type 5 (CAPN5) gene, tryptase 4 gene CC and sialoglycoprotease-like gene. Also described is a targeting construct CC (II), comprising a first polymucleotide sequence homologous to at least a CC first portion of PG, a second polymucleotide sequence homologous to at least a second portion of PG and a selectable marker. (II) is useful for CC producing a transgenic mouse comprising a disruption in a protease target CC gene, by introducing (II) into a cell, introducing the cell into a CC blastocyst, implanting the resulting blastocyst into a pseudopregnant CC mouse, where the pseudopregnant mouse gives birth to a chimeric mouse, CC useful for identifying an agent that modulates the expression or function of a protease target gene in (I) is modulated. (I) is also useful for testing the cfficacy of proposed genetic and pharmacological therapies for human CC efficacy of proposed genetic and pharmacological therapies for human
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06-DEC-2000;
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2000US-0251820P.
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Pred. No.:
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                                                                                                                                       GGTGGAAAAGCTATAGAACAGTTGGCCAAAGACGGAAATAGATTCCATTTTACTATCAAT
                                                                                                                                                      GlyGlyLysAlaIleGluHisLeuAlaLysGlnGlyAsnArgPheHisPheAspIleLys
                                                                                                                                                                                                                                                                    GlnGlyValSerAspPheLeuLeuGlyLysSerLeuAspIleAlaProGlyAspMet
                                                                                                                                                                                                                                                                                                                            ValGluPheProPheLeuValLeuLeuIleSerGlyGlyHisCysLeuLeuAlaLeuVal
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SerAlaAlaAspIleAlaAlaThrValGlnHisThrMetAlaCysHisLeuValLysArg
                            GATAAGCTAATAACACACAAGGAAAAAGAAGAAGGCATTGAGAAGGGGCAAATCCTGTCA
                                            AspLysIleIleMetLysLysGluLysGluGluGlyIleGluLysGlyGlnIleLeuSer
                                                                                   CCACCTATGCAGAATGCTAAGAATTGCGATTTTTCTTTCACGGGACTTCAACATATTACT
                                                                                                ProProLeuHisHisAlaLysAsnCysAspPheSerPheThrGlyLeuGlnHisValThr
                                                                                                                                                                                               CTTGACAAGGTGGCAAGAAGACTTTCTTTAATCAAACATCCAGAATGTTCTACAATGAGT
                                                                                                                                                                                                                 LeuAspLysValAlaArgArgLeuSerLeuIleLysHisProGluCysSerThrMetSer
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                                                                             New isolated nucleic acid encoding MP-1 protein, useful for preventing, treating, or ameliorating diseases associated with aberrant metalloproteinase activity, e.g. immune, metabolic, inflammatory and neurological disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   acquired immunodeficiency syndrome; AIDS; pulmonary disease; pneumoni emphysema; cystic fibrosis; vascular disorder; inflammatory disorder; neurological disorder; gene; ds.
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P-PSDB; ABG96487.
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10-APR-2001; 2001US-0282814P.
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Disclosure;

Page 462-463;

473pp; English

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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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AlaSerAsnPheTyrIleArgArgAlaLeuGluIleLeuThrAsnAlaThrGlnCysThr 347
                                                                                                                                                                                                                    CysLysGlnArgAspLeuLeuProGlnAsnAsnAlaValLeuValAlaSerGlyGlyVal
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The invention relates to a novel isolated human diagnostic and therapeutic polynucleotide (designated dithp). The novel dithp polynucleotide comprises: any of 188 DNA sequences consisting of 195-7798 base pairs fully defined in the specification; a polynucleotide comprising a naturally occurring polynucleotide sequence at least 90% identical to the dithp polynucleotide; a polynucleotide complementary to the dithp polynucleotide or its polynucleotide which is at least 90% identical; or an RNA equivalent of any of the polynucleotides mentioned above. The dithp polynucleotides have the following activities:

of 195-7798

Claim 1; or Alzheimer's.

SEQ ID NO 100; 634pp; English

antiarteriosclerotic, antiinflammatory, cerebroprotective, antilipaemic, antidiabetic, immunosuppressive, neuroprotective, nootropic, neuroleptic, tranquilizer, osteopathic, antiarthritic, antirheumatic, cytostatic,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diagnostic and therapeutic polynucleotide; dithp; antiarteriosclerotic; antiinflammatory; cerebroprotective; antilipaemic; antidiabetic; immunosuppressive; neuroprotective; nootropic; neuroleptic; tranquilizer; osteopathic; antiarthritic; antirheumatic; cytostatic; hepatotropic; virucide; haemostatic; anti-HIV; antithyroid; thyromimetic; dermatological; antibacterial; fungicide; antiparasitic; anticonvulsant; thrombolytic; anticoagulant; anorectic; vasotropic; antiulcer; gene therapy; protein replacement therapy; human; gene; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New human diagnostic and therapeutic polynucleotides and polypeptides, useful for diagnosing, treating or preventing e.g. leukemia, brain cancer, atherosclerosis, AIDS, thyroiditis, infections, obesity, stroke
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Peralta CH
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17-JAN-2002; 2002US-0349413P
17-JAN-2002; 2002US-0349946P
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                                                                                                                                                                                                                                                                                                                 The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABL9777-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
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                               standard;
                                                                                       AGCATTGATATCCAGGGCAGCGCGGGATTCGCC 1164
                                                                                                                  GlyValAspileSerLysGluValGlyGluAla 403
                                                                                                                                                                                                                                                                                         ArgArgAlaLeuGluIleLeuThrAsnAlaThrGlnCysThrLeuLeuCysProProPro
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                               CDNA; 1385
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27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                       complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises a 1'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of
                                                                                                                                                                                                                                                     the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the
                                                                                                                                                                                                               Sequence 1385
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Sugiyama T, Wakamatsu
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s defined in the specification. Where a primer set comprises:
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                 TATATTTGCCAAAGTATAGCATGTTTTATTCATTCAGGGGTTTTTTTGTTTTGTTAGTAAT
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                                                                                                                                                                                                                                                                    The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL040-ABL16175) and the encoded proteins (ABL5777-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated nucleic acid
genes from Drosophila and
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11-JUL-2000; 2000US-00614150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 25369; 21pp + Sequence Listing; English
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Search completed: June 16, 2005, 20:14:57 Job time : 636.5 secs	1465 TGATATCCAGGGCAGCGCGGATTCGCC 1438	394 lAspIleSerLysGluValGlyGluAla 403	1509AGCAT 1466	375 uGlyIleLeuHisAspIleGluGlyIleArgTyrGluProLysCysProLeuGlyVa 394

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Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlp
-MODEL=frame+ p2n.model -DEV=xlp
-Q=/cgp2_1/USPTO_spool_p/US10649273/runat_15062005_111418_6138/app_query.fasta_1.1429
-Q=/cgp2_1/USPTO_spool_p/US10649273/runat_15062005_111418_6138/app_query.fasta_1.1429
-DB=PublIshed_Applications_NA -QFMT=fastap_-SUFFIX=p2n.rnpb -MINMATCH=0.1
-LOOPEXT=0 -UNITS-bits -START=1 -ENU=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US10649273 @CGN 1 1 1034 @runat_15062005_111418_6138
-NCPU=6 -ICPU=3 -NO_MAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THEADS=1 -XCAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Maximum Match 10
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Ygapop 10.0 ,
Fgapop 6.0 ,
Delop 6.0 ,
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1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*

3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*

4: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*

5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*

6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
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Copyright (c) 1993 - 2005 Compugen Ltd
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/cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
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gn2-6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*
gn2-6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
gn2-6/ptodata/1/pubpna/USO9A_PUBCOMB.seq:*
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gn2-6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*
gn2-6/ptodata/1/pubpna/USOA_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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RESULT 1 US-10-067-4 Sequence FUNCAL 1 GENERAL 1 GENERAL 1 FUTLE OI FUTLE RE	444443333333326444444443346444444444444	Result No.
ULT 1 10-067-443-1 10-067-443-1 equence 1, Applicat ublication No. US20 ENERAL INFORMATION: APPLICANT: Bristol- TITLE OF INVENTION: TITLE OF INVENTION: FILE REFERENCE: DOO CURRENT APPLICATION CHERENT APPLICATION	21125 2125 2090.5 2090.5 2090.5 2090.5 2090.5 2090.5 20988 11944 11946.5 11186.5 1186.	Score
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ALIGNMENTS 067443 A1 ibb Company EOTIDE ENCODING A NOVEL CORD, MP-1 US/10/067,443	US-10-67-443-1 US-10-649-273-1 US-10-649-273-1 US-10-469-273-1 US-10-649-273-21 US-10-649-273-21 US-10-649-273-21 US-10-649-273-21 US-10-617-722-1 US-10-617-722-21 US-10-617-723-860-7447 US-10-617-723-860-7447 US-10-651-722-23 US-10-651-722-23 US-10-651-722-23 US-10-651-722-23 US-10-651-722-23 US-10-649-273-20 US-10-649-273-20 US-10-649-273-20 US-10-649-273-20 US-10-649-273-30 US-10-649-273-30 US-10-649-273-30 US-10-649-273-30 US-10-67-787-38 US-10-67-787-38 US-10-67-787-38 US-10-67-787-38 US-10-67-787-38 US-10-67-787-38 US-10-67-787-38 US-10-67-787-38 US-10-282-122A-26972 US-10-282-122A-3016 US-10-282-122A-3016 US-10-282-122A-3254 US-09-815-242-6696 US-10-282-122A-3259 US-09-815-242-6968 US-10-282-122A-32020 US-10-282-122A-32030 US-10-282-122A-3118 US-10-282-122A-3118 US-10-282-122A-15870 US-10-282-122A-15870 US-10-282-122A-15870 US-10-282-122A-15870 US-10-282-122A-15870 US-10-282-122A-15870 US-10-282-122A-15870 US-10-282-122A-19230 US-10-282-122A-19230 US-10-282-122A-19230 US-10-282-122A-19230 US-10-282-122A-19230	ID .
METALOPROTEASE HIGHLY EX	Sequence 1, Appli Sequence 1, Appli Sequence 21, Appli Sequence 21, Appli Sequence 21, Appli Sequence 21, Appli Sequence 21, Appli Sequence 400, Appli Sequence 400, Appli Sequence 23, Appli Sequence 23, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli Sequence 240, Appli Sequence 26972, Appli Sequence 316474, Appli Sequence 31015, Appli Sequence 31015, Appli Sequence 31015, Appli Sequence 31015, Appli Sequence 31015, Appli Sequence 31015, Appli Sequence 4007, Appli Sequence 4007, Appli Sequence 4007, Appli Sequence 4007, Appli Sequence 4007, Appli Sequence 4010, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 3119, Ap Sequence 3119, Ap	ΙĖ

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APPLICANT: Bristol-Myers Squibb Company
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE HIGHLY EXPRESSED
TITLE OF INVENTION: SPINAL CORD, MP-1
FILE REFERENCE: D0073 NP
CURRENT APPLICATION NUMBER: US/10/067,443
CURRENT FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 50/265,510
PRIOR PILING DATE: 2001-02-05
PRIOR PILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR PILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
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Best Local Similarity:
Query Match:
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; NAME/KEY: CDS
; LOCATION: (231)..(1472)
US-10-067-443-1
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SEQ ID NO 1
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TYPE: DNA
ORGANISM: Homo
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                                          ProProLeuHisHisAlaLysAsnCysAspPheSerPheThrGlyLeuGlnHisValThr
                                                                             GGTGGGAAAGCCATAGAACATTTGGCCAAACAAGGAAATAGATTTCATTTTGACATCAAA
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Sequence 1, Application US/10649273

Publication No. US20040043407A1

GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A N
FILE REFERENCE: D0073 CTT
CURRENT APPLICATION NUMBER: US/10/649,273
CURRENT FILING DATE: 2003-08-27
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 10/067,443
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SOFTWARE: PATENTIN PATENTIN OF SEC ID NOS: 71
SOFTWARE: PATENTIN VERSION 3.2
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Best Local Similarity:
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TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (231)...(1472)
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Best Local Similarity:
Query Match:
DB:
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TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A
FILE REFERENCE: D0073 DIV
CURRENT APPLICATION NUMBER: US/10/651,722
CURRENT FILING DATE: 2003-08-29
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 10/067,443
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
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Score:
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Publication No. US20040048302A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo
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US-10-480-988-36

; Sequence 36, Application US/10480988

; Publication No. US20050069877A1

; GENERAL INFORMATION:

; APPLICANT: GANDHI, Ameena R.; KABLE, Amy E.;

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APPLICANT: MASON, Patricia M.; GURURAJAN, Rajagopal;
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CURRENT APPLICATION NUMBER: US/10/480,988
CURRENT ETLING DATE: 2003-12-16
PRIOR APPLICATION NUMBER: US 60/300,508
PRIOR APPLICATION NUMBER: US 60/300,508
PRIOR APPLICATION NUMBER: US 60/303,445
PRIOR APPLICATION NUMBER: US 60/303,445
PRIOR APPLICATION NUMBER: US 60/303,445
PRIOR FILING DATE: 2001-07-06
PRIOR FILING DATE: 2001-07-06
PRIOR APPLICATION NUMBER: US 60/303,445
PRIOR APPLICATION NUMBER: US 60/303,445
PRIOR APPLICATION NUMBER: US 60/311,442
PRIOR APPLICATION NUMBER: US 60/311,42
PRIOR APPLICATION NUMBER: US 60/311,821
PRIOR APPLICATION NUMBER: US 60/314,821
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PRIOR APPLICATION NUMBER: US 60/314,821
PRIOR APPLICATION NUMBER: US 60/314,821
PRIOR APPLICATION NUMBER: US 60/314,821
PRIOR FILING DATE: 2001-08-24
PRIOR FILING DATE: 2001-08-29
PRIOR FILING DATE: 2001-08-29
PRIOR FILING DATE: 2002-05-03
NUMBER OF SEQ ID NOS: 56
SOFTWARE: PERL PROGRAM
ORGANISM: Homo sapiens
FEATURE:

PRIOR FILING DATE: SOME SEGURAL PROGRAMS
ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
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NAME/KEY: misc_feature
OTHER_INFORMATION: Incyte ID No:
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                                  AlaLeuSerLeuGlyValGlyLeuSerPheSerLeuGlnLeuValGlyGlnLeuLysLys 140
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Sequence 21, Application US/10067443

Publication No. US20030082782A1

GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEGTIDE ENCODING A N
TITLE OF INVENTION: SPINAL CORD, MP-1
FILE REFERENCE: DO073 NP
CURRENT APPLICATION NUMBER: US/10/067,443
CURRENT FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
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                GlyGlyLysAlaIleGluHisLeuAlaLysGlnGlyAsnArgPheHisPheAspIleLys
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PRIOR APPLICATION NUMBER: US 10/67,443
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PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SOUTWARE: PALENTIA US 50/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SEQ ID NO 21
LENGTH: 1387
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; ORGANISM: homo
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Sequence 21, Application US/10651722
Publication No. US20040048302A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
ITITLE OF INVENTION: POLYMUCLEOTIDE ENCODING A PILLE REFERENCE: DO073 DIV
CURRENT APPLICATION NUMBER: US/10/651,722
CURRENT FILING DATE: 2003-08-29
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 10/067,443
PRIOR PILING DATE: 2001-02-05
PRIOR FILING DATE: 2002-02-05
PRIOR FILING DATE: 2001-04-10
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SOFTWARE: PatentIn version 3.2
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Best Local Similari
Query Match:
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ORGANISM: homo
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 ProPheIleProIleHisHisMetGluAlaHisAlaLeuThrIleArgLeuThrAsnLys 160
                                                                                        AlaLeuSerLeuGlyValGlyLeuSerPheSerLeuGlnLeuValGlyGlnLeuLysLys
                                                                                                                                     ProAlaAlaGlnGlnLeuHisArgGluAsnIleGlnArgIleValGlnGluAlaLeuSer 100
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Sequence 1047, Application US/10887553A
Publication No. US20050085436A1
GENERAL INFORMATION:
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APPLICANT: Garza, Dan
APPLICANT: Li, Hao
TITLE OP INVENTION: Method to treat conditions associated
TITLE OP INVENTION: with insulin signalling dysregulation
FILE REPERENCE: 4-33262
CURRENT APPLICATION NUMBER: US/10/887,553A
CURRENT PILING DATE: 2001-07-09
FRIOR APPLICATION NUMBER: 60/485,883
PRIOR PILING DATE: 2003-08-07
NUMBER OF SEQ ID NOS: 1208
SOFTWARE: FastSEQ for Windows Version 4.0
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LENGTH: 1387
TYPE: DNA
ORGANISM: human
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                    GATAAAATAATAATGAAAAAGGAAAAAAGAGGAAGGTATATTTCTAATTAGTAAAGTTGAA
                                 AspLysIleIleMetLysLysGluLysGluGluGlyIle------
                                                                 CCTCCCTTGCATCATGCTAAAATTGTGATTTTTCTTTTACTGGACTTCAACACGTTACT
                                                                           ProProLeuHisHisAlaLysAsnCysAspPheSerPheThrGlyLeuGlnHisValThr
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98.38%
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Matches:
Conservative:
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Indels:
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Sequence 6, Application US/10012140

Publication No. US20030009017A1

GENERAL INFORMATION:

APPLICANT: Leiby, Kevin R.

APPLICANT: Kapeller-Libermann, Rosana

APPLICANT: Glucksmann, Maria A.

TITLE OF INVENTION: 14354 METHODS AND COMPOSITIONS OF HUMAN PROTEINS AND USES

TITLE OF INVENTION: 14354 METHODS AND COMPOSITIONS OF HUMAN PROTEINS AND CURRENT FILING DATE: 2001-11-08

PRIOR APPLICATION NUMBER: US/10/012,140

CURRENT FILING DATE: 2000-11-08

PRIOR APPLICATION NUMBER: 60/246,768

PRIOR APPLICATION NUMBER: 60/246,772

PRIOR FILING DATE: 2000-11-08

PRIOR FILING DATE: 2000-11-08

PRIOR FILING DATE: 2000-11-108

PRIOR FILING DATE: 2000-11-108

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PRIOR FILING DATE: 2000-11-108

PRIOR FILING DATE: 2000-11-108

PRIOR FILING DATE: 2000-11-108

PRIOR FILING DATE: 2000-11-15

NUMBER OF SEQ ID NOS: 49

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                      ; LENGTH: 1245
; TYPE: DNA
; ORGANISM: Homo :
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; LOCATION: (1)...(1820)
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US-10-012-140-4
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APPLICANT: Kapeller-Libermann, Rosana
APPLICANT: Glucksmann, Maria A.
TITLE OF INVENTION: 38650, 28472, 5495, 6550
TITLE OF INVENTION: 14544 METHODS AND COMPO
TITLE OF INVENTION: THEREOF
FILL REFERENCE: 381552004900
CURRENT APPLICATION NUMBER: US/10/012,140
CURRENT FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: 60/246,768
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: 60/246,772
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: 60/249,185
PRIOR APPLICATION NUMBER: 60/249,185
PRIOR FILING DATE: 2000-11-15
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ORGANISM: Homo
FEATURE:
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LOCATION: (146)...(1390)
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RESULT 11
US-10-094-749-400
                 Sequence 400, Application US/10094749
Publication No. US20030219741A1
GENERAL INFORMATION:
APPLICANT: ISOGAI, TAKAO
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: WAKAMATSUJ, AI
APPLICANT: WAKAMATSUJ, AI
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; TYPE: DNA
; ORGANISM: Homo s
US-10-094-749-400
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TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
FILE REFERENCE: 08435/0160
CURRENT APPLICATION NUMBER: US/10/094,749
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 60/350,435
PRIOR FILING DATE: 2002-01-24
PRIOR PILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: JP 2001-328381
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 3381
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SEQ ID NO 400
LENGTH: 2208
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NAGAI, KEIICHI
IRIE, RYOTARO
ValGluPheProPheLeuValLeuLeuIleSerGlyGlyHisCysLeuLeuAlaLeuVal
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YOSHIKAWA, TSUTOMU
OTSUKA, MOTOYUKI
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APPLICANT: Aziz, Natasha
APPLICANT: Ginsburg, Wendy M.
APPLICANT: Ziotnik, Albert
TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compos
TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modu
FILE REFERENCE: 05882.0193.NPUS01
CURRENT APPLICATION NUMBER: US/10/723,860
CURRENT FILING DATE: 2003-11-26
PRIOR APPLICATION NUMBER: 60/429,739
PRIOR APPLICATION NUMBER: 60/429,739
PRIOR FILING DATE: 2002-11-26
NUMBER OF SEQ ID NOS: 8393
SOFTWARE: PATENTIAL VERSION 3.2
SEQ ID NO 7447
LENGTH: 2890
TYPE: DNA
CREAKER DATE: 2003-21-26
TYPE: DNA
CREAKER DATE: 2003-21-26
TYPE: DNA
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ORGANISM: Homo sapiens FEATURE: NAME/KEY: misc_feature
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74 LysThrGlyGlyIleValProProAlaAla :::	Alignment Scores: 1.07e-201 Length: 1416 Pred. No.: 1747.00 Matches: 340 Score: 1747.00 Matches: 340 Percent Similarity: 100,00% Conservative: 1 Best Local Similarity: 99.71% Mismatches: 0 Query Match: 82.21% Indels: 0 DB: Gaps: 0 US-10-649-273-2 (1-414) x US-10-120-988-177 (1-1416)	; NUMBER OF SEQ ID NOS: 441 ; SOFTWARE: pt FL_genes Version 2.0 ; SEO ID NO 177 ; LENGTH: 1416 ; TYPE: DNA ; ORGANISM: Homo sapiens ; FEATURE: ; NAME/KEY: CDS ; LOCATION: (205)(1305) US-10-120-988-177	ng, man TIO TIO TIO TIO DA	няк, і о	2081 381 2093 401	Db 1961 CTGGTTGCATCTGGTGGTGTCGCAAGTAACTTCTGTATCCGCAGAGCTCTGGAAATTTTA 2020 Qy 341 ThrAsnAlaThrGlnCysThrLeuLeuCysProProProPedeuCysThrAspAsnGly 360 Db 2021 ACAAACGCAACAGTGCACTTTGTTGTGTCCTCCTCCCAGACTATGGCACTGATAATGGC 2080 Qy 361 IleMetIleAlaTrpAsnGlyIleGluArgLeuArgAlaGlyLeuGlyIleLeuHisAsp 380	Qy 301 ThrHisArgAlaIleLeuPheCysLysGlnArgAspLeuLeuProGlnAsnAsnAlaVal 320
RESULT 14 US-10-067-443-23 ; Sequence 23, Application US/10067443 ; Publication No. US20030082782A1 ; GENERAL INFORMATION: ; APPLICANT: Bristol-Myers Squibb Company ; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE HIGHLY EXPRESSED II ; TITLE OF INVENTION: SPINAL CORD, MP-1 ; PILE REFERENCE: D0073 NP ; CURRENT APPLICATION NUMBER: US/10/067,443	Qy 394 ValAspileSerLysGluValGlyGluAlaSerIleLysValProGlnLeuLysMetGlu 413	Qy 334 ArgArgAlaLeuGluIIeLeuThrAsnAlaThrGlnCysThrLeuLeuCysProProProProProProProProProProProProProP	GÁGAÁGGGCÁAÁTCCTGTCTTCAGCAGCAGACATTGCTGCCACAGTACAGCACACATG AlaCysHisLeuValLysArgThrHisArgAlaIleLeuPheCysLysGlnArgAspLeu	Oy 234 ArgPheHisPheAsplieLysProProLeuHisHisAlalysAshcysAspPheSetPhe 253	194 AspIleAlaProGlyAspMetLeuAspLysValAlaArgArgLeuSerLeuIleLysHis	Oy 154 ThrileArgLeuThrAsnLysValGluPheProPheLeuValLeuLeuIleSerGlyGly 173	Db 400 ACTACCATAAAACCAGGACTTAAGCCTTAAGCCTTGGGAGTGGGCTTATCATTTAGCTTACAG 459 Qy 134 LeuValGlyGlnLeuLysLysProPheIleProIleHisHisMetGluAlaHisAlaLeu 153

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CURRENT FILING DATE: 2002-02-05;
PRIOR APPLICATION NUMBER: US 60/266,518;
PRIOR FILING DATE: 2001-02-05;
PRIOR FILING DATE: 2001-04-10;
NUMBER OF SEQ ID NOS: 71;
SOFTWARE: Patentin version 3.0
SEQ ID NO 23;
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ProLysCysProLeuGlyValAspIleSerLysGluValGlyGluAlaSerIleLysVal 407
                                                                  | IleGluargLeuargAlaGlyLeuGlyIleLeuHisAspIleGluGlyIleArgTyrGlu
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GENERAL INFORMATION:

APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A P
FILE REFERENCE: D0073 CNT
CURRENT APPLICATION NUMBER: US/10/649,273
CURRENT FILING DATE: 2003-08-27
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 10/067,443
PRIOR APPLICATION NUMBER: US 0/067,443
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SOFTWARE: PATENTIN PATENTIN 3.2
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; TYPE: DNA
; ORGANISM: homo s
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                              GluLysGluGluGlyIleGluLysGlyGlnIleLeuSerSerAlaAlaAspIleAlaAla
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CysLysGlnArgAspLeuLeuProGlnAsnAsnAlaValLeuValAlaSerGlyGlyVal
                                                                                            GAAAAAGAGGAAGGTATTGAGAAGGGGCAAATCCTGTCTTCAGCAGCAGACATTGCTGCC
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	781 CCACAATTAAAAATGGAGATA 801	Db 78:	
	ProGlnLeuLysMetGluIle 414	Оу 408	_
A 780		Db 721	
1 407	ProLysCysProLeuGlyValAspIleSerLysGluValGlyGluAlaSerIleLysVal 407	Оу 388	_
A 720	ATTGAAAGACTACGTGCTGGCTTGGGCATTTTACATGACATAGAAGGCATCCGCTATGA	Db 661	
u 387	387 IleGluArgLeuArgAlaGlyLeuGlyIleLeuHisAspIleGluGlyIleArgTyrGlu	Qу 368	_
T 660	1 TTGTTGTGTCCTCCTCCCAGACTATGCACTGATAATGGCATTATGATTGCATGGAATGG	Db 601	
Y 367	LeuLeuCysProProProArgLeuCysThrAspAsnGlyIleMetIleAlaTrpAsnGly 367	Оу 348	_
T 600	1. GCAAGTAACTTCTATATCCGCAGAGCTCTGGAAATTTTAACAAACGCAACACAGTGCAC	Db 54:	
Ir 347	328 AlaSerAsnPheTyrIleArgArgAlaLeuGluIleLeuThrAsnAlaThrGlnCysThr 347	Qy . 328	_
C 540		Db 481	

Search completed: June 17, 2005, 08:03:08 Job time: 2842.5 secs

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Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlp
-Q=/cgn2 1/USPTO_spool_p/US10649273/runat_15062005_111416_6030/app_query.fasta_1.1429
-Q=/cgn2 1/USPTO_spool_p/US10649273/runat_15062005_111416_6030/app_query.fasta_1.1429
-DB=GenEmbl -QFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -STARF1=1 -END=-1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEARSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10649273_GCGN_1 1.7742_grunat_15062005_111416_6030 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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ALIGNMENTS

Alignment Scores: Pred. No.: Score: Percent Similarity: Percent Similarity: Query Match:	TITLE JOURNAL FEATURES SOUICE ORIGIN	SOURCE ORGANISM REFERENCE AUTHORS	RESULT 1 AR541929 LOCUS DEFINITION ACCESSION VERSION VERSION
cores: ilarity: Similarity:	Wang,D. and Nucleic acid Patent: US Patent 1. /oz /mc	Unknown. Unknown. Unclassified. 1 (bases 1 to 1416) 1 Tang, Y.T., Zhou, P., Zhang, J., Zhao, Q.A.,	AR541929 Sequence 177 from paten AR541929 AR541929.1 GI:53934009
1.37e-126 1385.00 100.00% 100.00%	Wang,D. and Drmanac,R.T. Nucleic acids and polypeptides Patent: US 6743619-A 177 01-JUN-2004; Location/Qualifiers 1. 1416 /organism="unknown" /mol_type="genomic DNA"	l. to 1416) thou,P., Goodri	ct .
Longth: Matches: Conservative: Mismatches: Indels:	ides 11-JUN-2004; Ers m ⁿ C DNA ⁿ	<pre>Unknown. Unknown. Unclassified. 1 (bases 1 to 1416) 1 (bases 1 to 1416) Tang,Y.T., Zhou,P., Goodrich,R., Liu,C., Asundi,V., Ren,F., Zhang,J., Zhao,Q.A., Yang,Y., Xue,A.J., Wehrman,T., Wang,JR.,</pre>	US 6743619.
1416 267 0		Asundi,V., Vehrman,T.,	linear
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1 (bases 1 to 1526)
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Chen,J., Feder,J.N., Nelson,T.C., Krystek,S.R. and Polynucleotides encoding a novel metalloprotease, P
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Location/Qualifiers
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Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, B.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Boutfard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and mouse cDNA sequences
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human and mouse cDNA sequences
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Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Brinkley, C., Brooks, S.,
Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,
Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,
Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,
McDowell, J., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,
McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,
Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
Vonca, A., Paragraf, L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
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1 (bases 1 to 1908)
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Email: cgapbs-r@mail.nih.gov
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On Dec 19, 2003 this sequence version replaced
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/organism="Homo sapiens"
/mol type="mRNA"
/db xref="taxon:9606"
/clone="MGC:20293 IMAGE:4121450"
/tissue_type="Muscle, rhabdomyosarcoma"
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Chen, J., Feder, J.N., Nelson, T.C., Krystek, S.R. and Polynucleotides encoding a novel metalloprotease, Polynucleotides 4042041-A 1 04-NOV-2003;
Patent: US 6642041-A 1 04-NOV-2003;
Location/Qualifiers
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                                                                                             LeuSerLeuIleLysHisProGluCysSerThrMetSerGlyGlyLysAlaIleGluHis
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Chen, J., Feder, J.N., Nelson, T.C., Krystek, S.R. and Duclos, F. Polynucleotides encoding a novel metalloprotease, MP-1 Patent: US 6642041-A 21 04-NOV-2003;

Patent: US 6642041-A 21 04-NOV-2003;
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                                  MetGluAlaHisAlaLeuThrlleArgLeuThrAsnLysValGluPheProPheLeuVal
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         Direct Submission
Submitted (27-OCT-2000) Chen J.M., MRC Molecular Enzymology
Laboratory, The Babraham Institute, Babraham, Cambridge, CB:
UNITED KINGDOM
                                                                           sialoglycoprotease homologue 
Unpublished
                                                                                                                                    Homo sapiens
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                          Homo
                                                                                                                                                                                 AJ295148.1 GI:11071726 metallopeptidase; sialoglycoprotease
                                                                                                                                                                                                    Homo sapiens mRNA for putative & AJ295148
                                                                                                 Chen, J.M., Fortunato, M. and Barrett, A.J. Cloning and sequencing of a second human
                                                        Chen, J.M.
                                                                                                                                                                       Homo
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Location/Qualifiers
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Primates;
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ArgAlaIleLeuPheCysLysGlnArgAspLeuLeuProGlnAsnAsnAlaValLeuVal 175
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                                                                      TGCCTAAAAATAGCTGCTCATTTCTGCAGGTATGAGAAGGGGCAAATCCTGTCTTCAGCA
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24. .1343
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Patent: WO 02074960-A 6 26-SEP-2002;
Millennium Pharmaceuticals, Inc. (US)
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae
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/db_xref="taxon:9606"
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COMMENT
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                                                                                                                                                                                                                                                                                                         PEATURES
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Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Croshe, R.D.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Boutfard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Butterfield, Y.S., Kzzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
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Mus musculus
Mus musculus
                                                                                                                                                                                                                                                                                                                         Clone distribution: MGC clone distribution information can be founthrough the I.M.A.G.B. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 123 Row: d Column: 22
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 21312463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: nisc mgc@nhgri.nih.gov

Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,
Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,
Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,
McDowell, J., Pearson, R., Stantripop, S., Thomas, P.D., Touchman, J.W.,
Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
Young, A., Zhang, L.-H. and Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA Library Preparation: Life Technologies, cDNA Library Arrayed by: The I.M.A.G.E. Conso
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (15-SEP-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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1 (bases 1 to 1844)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Web site: http://www.nisc.nih.gov/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaithersburg, Maryland;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Institute, 31 Center Drive, Room 11A03,
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  /tissue_type="Mammary tumor metastatized to lung. To arose spontaneously from a senescent normal mammary (clonal) outgrowth infected with the virus MMTV." /clone_lib="NCI_CGAP_Lu29" /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                             mol_type="mRNA"
strain="CZECH II"
                                                                                                                                                                                                                                                  organism="Mus musculus"
                                                                                                                                         clone="MGC:67870 IMAGE:5012054"
                                                                                                                                                                  xref="taxon:10090"
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AlaSerAsnPheTyrIleArgArgAlaLeuGluIleLeuThrAsnAlaThrGlnCysThr
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RITPSDLSAIATTIKPGLALSLGVGLSPSLQLVNRFKKPPIPHMEAHALTIRLTNK
VEFPFLVLLISGGHCLLALVQGVSDFLLLGKSLDIAPGDMLDKVARRLSIIKHPECST
MSGGKAIEHLAKDGNRRHFTINPPMQNAKNCDPSFTGLQHITDKLJTHKEKEEGIEKG
QILSSAADIAAAVQHATACHLAKRTHRAILFCKQKNLLSPANAVLVVSGGVASNIYIR
KALEIVANATQCTLLCPPPRLCTDNGIMIAMNGIERLRAGLGVLHDVEDIRYEPKCPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="QRI7; Region: Metal-dependent proteases
possible chaperone activity [Posttranslational
modification, protein turnover, chaperones]"
/db_xref="CDD:COG0533"
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/db_xref="GI:34849664"
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Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

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McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Fahey, J., Helton, E., Ketteman, M., Wadan, A., Kodrigues, S.,

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Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences

DYNA, S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,

Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

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                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Susanna Chan, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
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Submitted (25-OCT-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIH-MGC Project URL: http://mgc.nci.nih
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Institute, 31 Center Drive, Room 11A03,
                                                                                                                                                                                                                                nfo@bcgsc.bc.ca
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                          CysLysGlnArgAspLeuLeuProGlnAsnAsnAlaValLeuValAlaSerGlyGlyVal 180
                                                                                                                                                                                                   ThrValGlnHisThrMetAlaCysHisLeuValLysArgThrHisArgAlaIleLeuPhe 160
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/mol type="mRNA"
/strain="PVB/N"
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/db xref="taxon:5559"
/cione="IMAGE:5053559"
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/clone_lib="NCI_CGAP_Li9"
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Patent: EP 1293569-A 400 19-MAR-2003;
Helix Research Institute (JP) ; Resea
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Yamamoto,J.I., Isono,Y., Hio,Y., Otsuka,K., Nagai,K., Irie,R.,
Tamechika,I., Seki,N., Yoshikawa,T., Otsuka,M., Nagahari,K. and
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Ota, T., Suzuki, Y., Nishikawa, T., Otsuki, T., Sugiyama, T., Irie, R., Wakamatsu, A., Hayashi, K., Sato, H., Nagai, K., Kimura, K., Makita, H., Ishii, S., Yamamoto, J., Saito, K., Kawai, Y., Isono, Y., Nakamura, Y., Nagahari, K., Murakami, K., Yasuda, T., Iwayanagi, T., Wagatsuma, M., Shiratori, A., Sudo, H., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H., Sugawara, M., Takahashi, M., Kanda, K., Yokoi, T., Furuya, T., Kikkawa, E., Cmura, Y., Abe, K., Kamihara, K., Katsuta, N., Sato, K., Tanikawa, M., Yamazaki, M., Ninomiya, K., Ishibashi, T., Yamashita, H., Murakawa, K., Fujimori, K., Tanai, H., Kimata, M., Watanabe, M., Hiraoka, S., Chiba, Y., Ishida, S., Ono, Y., Takiguchi, S., Watanabe, S., Yosida, M., Hotuta, T., Kusano, J., Kanehori, K., Takahashi-Fujii, A., Hara, H., Tanase, T., Momura, Y., Togiya, S., Komi, F., Hara, R., Takeuchi, K., Arita, M., Imose, N., Musashino, K., Yuuki, H., Oshima, A., Sasaki, N., Aotsuka, S., Yoshikawa, Y., Matsunawa, H., Ichihara, T., Shiohata, N., Sano, S., Moriya, S., Momiyama, H., Satoh, N., Takami, S., Terashira, H., Watanabe, T., Sugiyama, A., Takemoto, M., Kawakami, B., Yamazaki, M., Watanabe, T., Sugiyama, A., Takemoto, M., Kawakami, B., Yamazaki, M., Watanabe, K., Kumagai, A., Itakura, S., Fukuzumi, Y., Fujimori, Y., Komiyama, M., Komatay, T., Ono, T., Yamada, K., Pujii, Y., Ozaki, K., Hirao, M., Ohmori, Y., Kawabata, A., Hikiji, T., Kobatake, N., Inagaki, H., Watanabe, M., Satoh, T., Shigeta, K., Senba, T., Matsumura, K., Nakajima, Y., Matsumura, K., Nakagawa, T., Ono, T., Yamashita, R., Nakajima, Y., Takahashi, Y., Nakagawa, K., Okumura, K., Nakagawa, T., Ohara, O., Isogai, T. and Sugano, S.
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Isogai,T., Otsuki,T. and Sugiyama,T.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (24-OCT-2001) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Jap
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Nat. Genet. 36 (1), 40-45 (2004)
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LeuLeuGlyLysSerLeuAspIleAlaProGlyAspMetLeuAspLysValAlaArgArg
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                                                                                                CTTTTGATTTCTGGAGGTCACT
                                                                                                                                                                                           ATGGAGGCTCATGCACTTACTATTAGGTTGACCAATAAAGTAGAATTTCCTTTTTTAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /protein_id="bab70923.1"
//db_xref="G1:16550167"
//db_xref="G1:16550167"
//db_xref="G1:16550167"
//tanslation="millitkyacyperceskervybeplrsenhepgtlelhkivlgiet
scddtaaavvdbtgnvlgbaihsqtbyhlkytggivppaaQQlhreniQRivQbalsas
gvsebdlsalatikpclalicyglspslolygolkkpfiphhybahaltirlkhbets
GvsebdlsalatikpclalivQgyspflllgksldiapghudxvarrlelikhbetst
vEppflvllisgghcllalvQgyspflllgksldiapghudxvarrlelikhbetst
MSGGKAlbhlakQGNRPHFDIKpblhhakNCDbppfGLQhVTDKIIMKXBKEBGIEKG
QILSSAADIAATVQHYMACHLVKRTHBAILFCKQRDLLPQNNAVLVASGGVASNFCIR
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/db xref="taxon:9606"
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clone_lib="FEBRA2"
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Strausberg, R.L., Peingold, E.A., Grouse, L.H., Derge, J.G.,

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Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, B.D.,
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BC078974
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Mammalia; Eutheria; Rodentia;
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Submitted (02-AUG-2004) National Institutes of Health, Mammalian Sene Collection (MGC), Cancer Genomics Office, National Cancer Gene Collection (MGC), Cancer Genomics Office, National Cancer Gene Collection (MGC), Cancer Genomics Office, National Cancer Gene Collection (MGC), Cancer Genomics Office, National Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer General Cancer G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
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Tissue Procurement: Howard J
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                                                                                                                                                                                                                                                                                                                                                                                                                              /product="Tinknown (protein for IMAGE:7111906)"
/protein_id="AAH78974.1"
/db_xref="GI:50925880"
/translation="MLMLSKTAGAIPRPPRSNVRGFIRRENVQPRALFHHKLVLGIET
SCDDTAAAVUDETGNVLGEALHSQTEVHLKTGGIVPPVAQQLHRENIQRIVEEALSAS
GVSPSDLSAIATTIKPGLALSLGVGLSFSVQLVNQFKKPFIPHHMEAHALTIRLTHK
VGFPFLVLLISGGHCLLALVQSVSDFLLLGKSLDIAFGDMLDKVARRLSLIKHPECST
MSGGKAIEHLAKEGNRFHFTINPPMQNAKNCDFSFTGLQHVTDKLITHKEKEEGIEKG
QILSSAADIAAAVQHATACHLAKRTHRAILFCQQKNLLSPANAVLVVSGGVASNLYIR
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/clone_lib="NIH_MGC_237"
/lab_host="DH10B"
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/mol_type="mRNA"
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NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Marcello Bento Soares, |
cDNA Library Preparation: M. Bento Soares, |
cDNA Library Arrayed by: The I.M.A.G.E. Con
DNA Sequencing by: Institute for Systems Bi
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                                                                               Bento Soares, Ph.D.
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                AlaThrValGlnHisThrMetAlaCysHisLeuValLysArgThrHisArgAlaIleLeu
                                                                                                                                                                                                                                                                                                               LysGluLysGluGluGlyIleGluLysGlyGlnIleLeuSerSerAlaAlaAspIleAla 139
                                                                                                                                                                                                                                                                                                                                                                                                        LysAsnCysAspPheSerPheThrGlyLeuGlnHisValThrAspLysIleIleMetLys
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                                                                                                                                                                                                   GCTGCGGTACAGCATGCAACAGCGTGCCACCTTGCGAAAAAGAACACATCGCGCTATTCTG
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/clone="IMAGE:1327545"
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/strain="C57BL/6J"
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672 199 612 179 159 492

552

372 99 312 79 252 59

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contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton,
Madan, Stephanie Rodrigues, Amy Sanchez
      Mark Ketteman, Anuradha and Michelle Whiting
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Clone distribution: MGC clone distribution information can through the I.M.A.G.E. Consortium/LLML at: http://image.llr Series: IRAK Plate: 113 Row: b Column: 1
This clone was selected for full length sequencing because passed the following selection criteria: Hexamer frequency analysis. http://image.llnl.gov information can be because it requency ORF

TCTGGTTTGAAACTGACTTGGTCAATAGTGGGTTATCTTTGTCTTAAT------AAT 192 LeuAlaLeuValGlnGlyValSerAspPheLeuLeuLeuGlyLysSerLeuAsp /tissue_type="Thymus gland, mouse" /clone_lib="Soares_thymus_2NbWT" /lab_host="DHIOB" /note="Vector: pT7T3D-Pac" Conservative: Mismatches: Indels: BC051211 (1-1109) 1109 190 22 35 21 -ValAlaArg

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Submitted (02-FEB-2004) Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. B-mail enquiries: chickest@bms.umist.ac.uk
BBSRC/Dundee/Nottingham/Sanger/Sheffield/UMIST Gallus gallus cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BBSRC/Dundee/Nottingham/Sanger/Sheffield/UMIST cDNA collection, from a library constructed by Elizabeth Bosch. cDNA was prepared from RNA extracted from muscle, normalised, and poly A-trimmed. ECORI-NotI cut cDNA was then ligated into the vector. Vector: pBluescript II KS(+); Site_1: EcoRI; Site_2: NotI Host: Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequencing project.
This sequence is for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Boardman, P.B., Bonfield, J.K., Brown, W.R.A., Carder, C., Chalk, S.E., Croning, M.D.R., Davies, R.M., Francis, M.D., Grafham, D.V., Croning, M.D.R., Lumphray, S.J., Hunt, P.J., Maddison, M., McLaren, S.R., Hubbard, S.J., Overton, I.M., Rogers, J., Scott, C.E., Taylor, R.G.,
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1 (bases 1 to 1522)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
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Gallus gallus
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 LeuLeuIleSerGlyGlyHisCysLeuLeuAlaLeuValGlnGlyValSerAspPheLeu
                                    MetGluAlaHisAlaLeuThrIleArgLeuThrAsnLysValGluPheProPheLeuVal
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                                                                                                                                                                                                                                                                                                /clone_lib="CSEQRBN11"
/dev_stage="adult"
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/clone="ChEST189i14"
                                                                                                                                                                                                                                                                                                                                                                       organism="Gallus gallus"
/mol_type="mRNA"
/strain="Layer and broiler"
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CCAAGACTAAGG 1378
                                 ProGlnLeuLys 264
                                                                       CCAAAAGCTCCCCTTGGAATTGATATTTCCAAAAGAGTTGAAGAGGATTCCATCAAAGTG
                                                                                                                                               ATTGAAAGGTTGCGTGCAGGATGTGGTATTTTATACAGTACTGATGGCATCCGCTACGAA
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Search completed: June 16, 2005, 23:18:39 Job time: 3202.26 secs

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Run
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-MODEL=frame+ p2n.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/US10649273/runat_15062005_111415_6022/app_query.fasta_1.1429
-Q=/cgn2_1/USPTO_spool_p/US10649273/runat_15062005_111415_6022/app_query.fasta_1.1429
-DB=N_Geneseq_16Dec04 -QFMT=fastap -SUFFIX=p2n.rng -MIMMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=sct -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10649273_aCGN 1 1 1063 @runat 15062005_111415_6022 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-USER-US10649273_aCGN 1 1063 @runat 15062005_111415_6022 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0% Maximum Match 10
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                                                                                                                                                                                                                                                                                                                                              Database :
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                                                                                                                                                                                                                                                                                                                                                                                                    FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Ygapop 10.0 ,
Fgapop 6.0 ,
Delop 6.0 ,
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11:
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Listing first 45 summaries
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Aas56045 Salmonell	AAS56045	4	1014	20.2		44
6	_	10	1074	20.3		43
77	ACA44384	æ	1020	20.3		42
Adt05644 Haemophil	ADT05644	13	85814	20.4	282.5	41
		13	9967		N	40
Abv61069 Human pro	ABV61069	Ç	372		æ	39
Continuation (6 of	AAT42063_05	N	110000		•	38
Aca34150 Prokaryot	ACA34150	œ	1029	٠	•	37
Aas53309 Haemophil	AAS53309	4	1029	•	•	36
w		10	1026	٠	289.5	ω 5
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Ä		11	1059	٠	291.5	ω u
Adg73341 P aerugin		10	1026	21.0	291.5	32
ŭ	ACA42146	œ	1026	21.0		31
Aas54064 Pseudomon	AAS54064	4.	1026	21.0	291.5	
Abq90383 M. capsul	ABQ90383	6	1092	•	300	
	ABK37804	σ	1000	•		28
Aaf91424 Moraxella	AAF91424	4.	1000	21.8	301.5	
	ACA43173	œ	1032	22.0	304.5	26
0		12	1053	22.2	0	25
Genomic f	AAF28551	4	94750	22.3		24
Prokaryo	ACA39102	œ	1044	22.3	٠	23
	ACA20445	œ	936	•		
	ACA26804	œ	1146	•	•	
	AAH15110	4	1385	24.4	338.5	20
	AAD48239	σ	4360		342	19
4	AAC38454	w	1557	•	•	18
	ABL24632	4.	3656	•		17
	⊳	4.	1601	•	415.5	91
6 DNA up-r		12	371		468	15
S		12	371	•	468	4
Aas84622 DNA encod	AAS84622	v	2734	•	599	13
Abq75508 Murine si	×	σ	1572	•	983	12
5 Human		10	3358	۳	995.5	11
Adq24627 Human sof		12	2890	٠	1204	10
2 Human		10	20	ণ	1204	ω
20 cDNA e	ABS	10	2	97.3	1348	80
60887	880	œi.	N	97.3	1348	7
Aad46856 Human gly	AAD46856	σ	1820	97.3	1348	0

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ALIGNMENTS

RESULT 1 ABX70950 ID ABX7

ABX70950 standard; cDNA; 1416 BP.

ABX70950;

Novel human cDNA sequence #175.

Human; gene; ss; nervous system disorder; peripheral neuropathy; Huntington's disease; amyotrophic lateral sclerosis; haemophilia; neurodegenerative disease; Parkinson's disease; Alzheimer's disease; autoimmune disease; systemic lupus erythematosus; rheumatoid arthritis; insulin-dependent diabetes mellitus; anaemia; thrombocytopaenia; wound; ulcer; burn; bone disorder; osteoporosis; osteoatrhitis; stroke; fibrosis; reperfusion injury; infection; allergic rhinitis; asthma; coagulation disorder; cancer; tumour; inflammatory disease; septic shock; Crohn's disease; anaphylaxis; proliferation; chemotactic; differentiation; stem cell growth factor; haematopoiesis; chemokinetic; haemostatic; antiinflammatory; expressed sequence tag; EST.

Homo sapiens.

wozgoogsi711-A2.
17-OCT-2002; 2002WO-US001222.

Result No.

Score

Match

Length

B

Description

1385 1385 1385

100.0 100.0 100.0 100.0

1416 1526 2058 2197 2572

> ABX70950 ABS76639 ABA93268 ABS76635

Abx70950 Novel hum
Abs76639 DNA encod
Abs93268 Human O-s
Abs76635 DNA encod
Abt23207 Human pro

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CC diseases (e.g. peripheral neuropathy, Huntington's disease, amyotrophic (c) lateral sclerosis); neurodegenerative diseases (e.g. Parkinson's disease, Alzheimer's disease); autoimmune disease (e.g. systemic lupus (c) Alzheimer's disease); autoimmune disease (e.g. systemic lupus (c) Huntington's disease); autoimmune disease (e.g. systemic lupus (c) Huntington's disease); autoimmune disease (e.g. systemic lupus (c) Huntington's disease); autoimmune disease (e.g. systemic lupus (c) Huntington's (e.g. systemic mellitus); (c) Huntington's (e.g. shaemia and thrombocytopaenia); (c) wounds, ulcers, burns; bone disorders (e.g. stroke, head (c) trauma); lung or liver fibrosis; reperfusion injury in various tissues; (c) bacterial, viral or fungal infections; allergic conditions such as (c) bacterial, viral or fungal infections; allergic conditions such as (c) allergic rhinitis, asthma; coagulation disorders (e.g. haemophilia); (c) cancer and tumours; and inflammatory diseases (e.g. septic shock, Crohn's (c) disease, anaphylaxis). The protein may be used to inhibit the growth, (c) viruses, or to effect bodily characteristics, biorhythms or circadian (c) viruses, or to effect bodily characteristics, biorhythms or circadian (c) control or function of infections and control or circadian (c) viruses, or to effect bodily characteristics, biorhythms or circadian (c) control or control or control or control or control or control or control or control or control or control or control or control or control or control or control or control or control or control or control or control or control or control or control or control or control or control or control or control or control or control or control or control or control or control or control or control or control or control or control or control or control or control or control or control or control or control or control or control or control or control or control or control or control or control or control or control or control or control or control or control or control or co
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention relates to the cDNA sequences encoding an isolated nove human polypeptide. The protein encoded by the nucleic acid of the human invention is useful for treating central and peripheral nervous system invention is useful for treating central and peripheral nervous system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page; 612pp; English.
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GOODRICH R W.
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Yang Y,
LeuAlaLysGlnGlyAsnArgPheHisPheAspIleLysProProLeuHisHisAlaLys
                                                                                                          LeuSerLeuIleLysHisProGluCysSerThrMetSerGlyGlyLysAlaIleGluHis
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                                                                                                                 05-FEB-2001;
10-APR-2001;
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Chen J,

Feder J,

Nelson TC,

Duclos

Ή,

Krystek

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New isolated nucleic acid encoding MP-1 protein, useful for preventing, treating, or ameliorating diseases associated with aberrant metalloproteinase activity, e.g. immune, metabolic, inflammatory and
                                                                                                                                                                                                                        WPI; 2002-723329/78 P-PSDB; ABG96487.
                                                                                                                                                             Disclosure; Page 462-463; 473pp; English.
                                                                                                                                                                             neurological disorders.
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an

amystrophic lateral sclerosis (ALS), its juvenile form or an ALS-like condition. The compositions and methods are also useful for diagnosing, prognosticating, treating, ameliorating and/or treating disorders associated with Mp-l activity, e.g. diabetes, cancer, reproductive disorders (e.g. Kleinfelter's syndrome, genital warts, or germinal cell aplasia), metabolic disorders (e.g. premature puberry, Kallman syndrome, or Cushing's syndrome, neurodegenerative diseases (Alzheimer's disease, Parkinson's disease, Huntington's disease or Tourette syndrome), liver and renal diseases and immune disorders (e.g. AIDS, rheumatoid arthritis or sepsis), pulmonary diseases (e.g. pneumonia, emphysema or cystic fibrosis) and vascular, inflammatory and neurological disorders (e.g. AIZheimer's disease or Parkinson's disease). This sequence represents a Alzheimer's disease or Parkinson's disease). metalloprotease (MP-1). (I) is useful for preventing, treating, or ameliorating a medical condition, particularly an immune disorder, aberrant glutamate transport or motor neuron disorder, such as The invention describes an isolated nucleic acid molecule (I) encoding metalloprotease (MP-1). (I) is useful for preventing, treating, or metalloprotease MP1 polynucleotide

Sequence 1526 BP; 484 A; 297 ü 289 <u>ი</u> 456 7 0 ₽, 0 Other;

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The present sequence encodes human O-sialoglycoproteinase-like protein (OSGPLP). The present invention also describes: (1) the preparation of the OSGPLP protein; (2) applying the OSGPLP protein in diagnosis; (3) the prevention and/or treatment of related diseases; (4) utilising the OSGPLP protein in screening its agonist, excitomotor and inhibitor and preparing an antihody against the OSGPLP protein; and (5) the use of the OSGPLP polynucleotide sequences, proteins, agonists, excitomotors, inhibitors and antibodies in treating diseases related to the abnormal OSGPLP gene and in preparing the medicine composite for the treatment

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/product= ."O-sialoglycoproteinase-like protein"
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Best Local Similarity:
ABS76635;
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11-DEC-2002
                        (first entry)
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encoding novel human metalloprotease MP1

Metalloprotease; MP-1; immune disorder; glutamate transport; cancer; motor neuron disorder; amyotrophic lateral sclerosis; ALS; diabetes; reproductive disorder; Kleinfelter's syndrome; germinal cell aplasia; genital wart; metabolic disorder; premature puberty; Kallman syndrome; cushing's syndrome; neurodegenerative disease; Alzheimer's disease; Parkinson's disease; Huntington's disease; Tourette syndrome; sepsis; liver disease; renal disease; immune disorder; rheumatoid arthritis; acquired immunodeficiency syndrome; AIDS; pulmonary disease; pneumonia; emphysema; cystic fibrosis; vascular disorder; inflammatory disorder; neurological disorder; gene; ds.

Homo sapiens.

19-SEP-2002.

05-FEB-2002; 2002WO-US003353

05-FEB-2001; 2001US-0266518P. 10-APR-2001; 2001US-0282814P.

(BRIM) BRISTOL-MYERS SQUIBB ၀

Feder J, Nelson TC, Duclos Ţ Krystek

2002-723329/78. DB; ABG96478.

New isolated nucleic acid encoding MP-1 protein, useful for preventing, treating, or ameliorating diseases associated with aberrant metalloproteinase activity, e.g. immune, metabolic, inflammatory and neurological disorders.

Fig 1A-C; English.

CC aberrant glutamate transport or motor neuron disorder, such as CC amyotrophic lateral sclerosis (ALS), its juvenile form or an ALS-like CC condition. The compositions and methods are also useful for diagnosing, prognosticating, treating, ameliorating and/or treating disorders CC associated with MP-1 activity, e.g. diabetes, cancer, reproductive CC disorders (e.g. Kleinfelter's syndrome, genital warts, or germinal cell CC aplasia), metabolic disorders (e.g. premature puberty, Kallman syndrome, CC or Cushing's syndrome), neurodegenerative diseases (Alzheimer's disease, CC Parkinson's disease, Huntington's disease or Tourette syndrome), liver CC and renal diseases and immune disorders (e.g. AIDS, rheumatoid arthritis CC or sepsis), pulmonary diseases (e.g. pneumonia, emphysema or cystic CC fibrosis) and vascular, inflammatory and neurological disorders (e.g. Alzheimer's disease or Parkinson's disease). This sequence represents a CC metalloprotease MP1 polynucleotide The invention describes an isolated nucleic acid molecule (I) encoding metalloprotease (MP-1). (I) is useful for preventing, treating, or ameliorating a medical condition, particularly an immune disorder, an

Sequence 2197 BP; 681 A; 441 Ç ç, 636 Ħ, 0 U; 0 Other;

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Alignment
Pred. No.:
                                                        Percent Similarity:
Best Local Similarity:
Query Match:
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                          US-10-649-273-2_COPY_148_414 (1-267)
                                                                                        Score:
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MetGluAlaHisAlaLeuThrIleArgLeuThrAsnLysValGluPheProPheLeuVal
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Conservative:
Mismatches:
Indels:
Gaps:
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RESULT 5
ABT23207
ID ABT2
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AC ABT2
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DT 01-W
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DT 01-W
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W Cytc
KW Cytc
KW Cytc
KW proto
KW proto
KW gastm
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KW gastm
  cérebroprotective; antiparkinsonian; nootropic; antiinflammatory; antiulcer; hepatotropic; gynaecological; antibacterial; virucide; protozoacide; antiparasitic; cell proliferative disease; pMOD; protein modification and maintenance molecule; immunogenic fragment; cancer; autoimmune; inflammatory disease; neurological disorder; gastrointestinal; developmental; vesicle trafficking disorder; infection; protein interaction; drug-target interaction; gene expression profile; human; gene; ds.
                                                                                                                                                                         Cytostatic; antiarteriosclerotic; anti-HIV; antiallergic; anticonvulsant;
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Percent Similarity:
Best Local Similarity:
Query Match:

1.09e-146 1385.00 100.00% 100.00%

Matches: Conservative: Mismatches: Indels:

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(1-2572)

Pred. No.:

2572

780 A; 489

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0 Other;

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The invention relates to an isolated polypeptide comprising: any of 28 CC sequences of 48-1256 amino acids; a natural amino acid sequence at least CC 90% identical to the 28 amino acid sequences, 94% identical to a sequence conformation of the 28 amino acid sequences, 94% identical to a sequence of 103 or 267 amino acids, 96% identical to a sequence of 414 amino acids, or 97% identical to a sequence of 242 amino acids, all given in CC the specification; or a biologically active or immunogenic fragment of the isolated polypeptide. The polypeptides and polymucleotides are useful in diagnosing, treating and preventing diseases or conditions associated with the decreased expression of protein modification and maintenance confocules (PMOD), such as cell proliferative diseases (e.g. cancer, catherosclerosis), autoimmune/inflammatory diseases (e.g. cancer, caplepsy), gastrointestinal (e.g. ulcer, cirrhosis), reproductive (e.g. callergies), neurological disorders (e.g. stroke, Parkinson's disease, condometriosis), developmental, vesicle trafficking disorders, and confoculated in assessing the effects of exogenous compounds on the expression of nucleic acid and amino acid sequences of PMOD. The PMOD or its craget polymucleotide and compounds for effectiveness as agonist or attagonist of the polypeptides, or in altering the expression of the capters of the polypeptides. The microarray is useful in monitoring compounds on the expression profiles. This polymucleotide sequence represents the DNA encoding a human PMOD protein of the invention
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Walia NK, Mason PM, Walia NK, Mason PM, S
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06-JUL-2001;
13-JUL-2001;
09-AUG-2001;
24-AUG-2001;
29-AUG-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 91; Page 211; 225pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diagnosing, treating and preventing diseases or conditions associated with the aberrant PMOD expression, e.g. cancer, AIDS, atherosclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated human PMOD polypeptide and polynucleotide, useful for diagnosing, treating and preventing diseases or conditions associated
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2001US-0311442P.
2001US-0314821P.
2001US-0315992P.
2002US-0378205P.
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son CH, Honchell CD, Nguyen DB, Lu DAM, Lee EA,
Barroso I, Ramkumar J, Griffin JA, Li JX, Yang
Gietzen KJ, Ding L, Baughn MR, Borowsky ML, Yan
son PM, Gururajan R, Lee S, Becha SD, Lee SY, T
Luo W, Sprague WW, Tang YT, Lu Y, Zebarjadian Y;
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Duggan BM; e EA, Yue l Yang J; IL, Yao MG; Tran UK;

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           Human; adenosine deaminase; seven transmembrane domain receptor; cancer; TTM; glycoprotease; immune disorder; IgA deficiency; allergy; arrhythmia; rheumatoid arthritis; diabetes; atherosclerosis; cardiovascular disorder; hyperrension; ischaemic heart disease; obesity; myocardial infarction; endothelial cell disorder; Grave's disease; psoriasis; brain disorder; Parkinson's disease; Alzheimer's disease; haematopoietic disorder;
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The present invention relates to novel 38650, 28472, 5495, 65507, 81588
CC or 14354 nucleic acid molecules which encode adenosine deaminase, glycocrotease or seven transmembrane domain (77M) receptor family members.
CC Sequences of the invention are useful in diagnosing and treating cancer
CC lung cancer), immune disorders (e.g. selective IgA deficiency, rheumatoid
CC arthritis, diabetes, allergy), heart or cardiovascular disorders (e.g.,
CC hypertension, atherosclerosis, arrhythmias, ischaemic heart disease,
CC myocardial infarction, thrombus) including endothelial cell disorders
CC (e.g. psoriasis, Grave's disease), haematopoietic disorders, brain
CC disorders (e.g. cerebral oedema, Parkinson's or Alzheimer's disease),
CC pain and metabolic disorders (e.g. obesity), liver disorders or platelet
CC (e.g. diagnostic assays, prognostic assays, monitoring clinical trials
CC (e.g. diagnostic assays, prognostic assays, monitoring clinical trials
CC and pharmacogenetics) and prophylactic and therapeutic methods. The
CC cused in order the assays also be used in chromosome mapping, tissue typing and
CC cused in core therapeutic methods. The
                                                                                                                                                                                                                                                                                                                                                                                                                                   New 38650, 28472, 5495, 65507, 81588 or 14354 nucleic acid molecules, useful for diagnosing and treating cancer, immune, cardiovascular, hematopoietic, brain, pain, metabolic, liver or platelet disorders, and in pharmacogenomics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-NOV-2000; 2000US-0246768P
08-NOV-2000; 2000US-0246772P
15-NOV-2000; 2000US-0249185P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     chromosome mapping; tissue typing; gene therapy; neuroprotective; cytostatic; anorectic; cardiant; haemostatic; gene; ss.
                                                    also used in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MILL-) MILLENNIUM PHARM INC
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/note= "This region is specifically
6 in claim 1 of the specification"
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Sequence 1820 вP; 543 A; 365 Ç 393 <u>ი</u> 518 Η. 0 ς, 1 Other; 밁 Ś 밁 δ 밁 Ś 밁 5 В Ś g. S 밁 Ś g Ş 밁 Ş В S 밁 S 멼

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                                                         US-10-649-273-2_COPY_148_414 (1-267) x AAD46856 (1-1820)
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Best Local Similarity:
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                                                                                                       1348.00
98.50%
97.38%
97.33%
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                                                                                                          Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                             Gaps:
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LeuLeuIleSerGlyGlyHisCysLeuLeuAlaLeuValGlnGlyValSerAspPheLeu

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RESULT 7
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                                                                                                                                                                                                                                                                                                                                     28472 encoding a glycoprotease.
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                                               Location/Qualifiers
  /product= "Glycoprotease"
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                                                                                                                                                                                                                                                                     Alignment Scores: Pred. No.:
                                                                                                                                                                                                                                                                                                                                  The invention relates to an isolated 38650 (encoding adenosine CC deaminase), 28472 (encoding a glycoprotease), 5495 (encoding a 7 CC transmembrane receptor), 65507, 81588 or 14354 nucleic acid molecule (or CC a sequence which is at least 60% identical to the six nucleic acids or CC naturally occurring variants, or a DNA insert of the plasmid deposited CC with the American Type Culture Collection as Accession No. not defined in CC the specification, which encodes the amino acid sequence). Also included are a host cell containing the nucleic acids (used to produce the protypeptide, and identifying a compound that binds to/modulates the CC activity of the polypeptide. The nucleic acid molecules, polypeptides and CC methods are useful for diagnosing, treating cancer, aberrant cellular CC proliferation and/or differentiation, immune disorders, heart disorders, CC cardiovascular disorders, blood vessel disorders, brain disorders, pain CC and metabolic disorders, blood vessel disorders, brain disorders, pain CC eamples of these disorders are given in the specification). The present cxx
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-NOV-2000;
08-NOV-2000;
15-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   molecules, useful for diagnosing, treating cancer, pain, or immune, heart, endothelial cell, hematopoeitic, blood vessel, brain, metabo and liver disorders.
                                                                                                                                                                                                                                                                                                              Sequence 1820
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(KAPE/) KAPELLER-LIBERMANN
(GLUC/) GLUCKSMANN M A.
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LeuLeuGlyLysSerLeuAspTleAlaProGlyAspMetLeuAspLysYelAlalampArg
                                                         CTTTTGATTTCTGGAGGTCACTGTCTGTTGGCATTAGTTCAAGGAGTTTCAGATTTTCTG
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/note= "Specifically claimed in
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The invention describes isolated 38650, 28472, 5495, 65507, 81588 and CC 14354 nucleic acid molecules (I) and their encoded polypeptides (II). The CR 38650 nucleic acid molecule comprises a sequence encoding adenosine CC deaminase. The 28472 nucleic acid molecule comprises a sequence encoding comprises a sequence encoding adenosine CC sequences that encode a human seven transmembrane domain (7TM). The CR 38650, 28472, 5495, 65507, 81588 and 14354 comprise CC sequences are useful for diagnosing, preventing or treating a subject CC with or at risk of developing a disorder, e.g. cancer or aberrant CC with or at risk of developing a disorder, e.g. cancer or aberrant. CC cellular proliferation and/or differentiation (e.g. breast, ovarian, CC prostate, colon or lung cancer), immune disorders, heart disorders, colon oversel disorders, manual disorders, heart disorders, colon oversel disorders, pain and metabolic disorders, CC liver disorders or platelet disorders. These disorders include carroinoma, constant, leukaemia, Hodgkin's disease, autoimmune disorders, Kawasaki CC sarcome, Raynaud's disease, aneurysm, cerebral ischaemia, peripheral consurpathy, Alzheimer's disease, Parkinson's disease, anorexia nervosa, constant, and chronostants.
                Alignment Scores:
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08-NOV-2000; 2000US-0246772P.
15-NOV-2000; 2000US-0249185P.
                                                        Sequence
                                                                                                                 neuropathy, Alzheimer's disease, Parkinson's disease, anorexia nervosa, cachexia or diabetes. This sequence encodes the novel human glycoprotease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 2; Fig 8A-B; 178pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81588 and 14354, useful for treating e.g. leukemias, Hodgkin's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New adenosine deaminase, glycoprotease and seven transmembrane domain nucleic acids and polypeptides, designated 38650, 28472, 5495, 65507,
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LeuLeuGlyLysSerLeuAspIleAlaProGlyAspMetLeuAspLysValAlaArgArg
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                            Isogai T, Sugiyama T,
Yamamoto J, Isono Y,
Seki N, Yoshikawa T,
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24-JAN-2002; 2002US-0350435P.
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Hio Y, Otsuka K, Nagai K, Irie
Otsuka M, Nagahari K, Masuho Y;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New polynucleotides encoding full-length polypeptides, e.g. secretory and/or membrane proteins, useful for developing medicines for diseases which the gene is involved, or as target molecules for gene therapy.
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US-10-649-273-2_COPY_148_414 (1-267) x ADQ24627 (1-2890)
                                             Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                          Alignment Scores
                                                                                                                                                                              which comprises obtaining a first soft tissue sample from an individual and a normal soft tissue sample from the same or different individual, determining the expression of a gene in both samples and comparing the expression of the gene in both soft tissue samples, where a higher level of protein expression in the first soft tissue sample indicates the presence of soft tissue sarcoma. The method of the invention has cytostatic applications and may be useful for detecting soft tissue sarcoma, possibly via gene therapy or vaccine production. The nucleic acid sequences may be useful in diagnostic and screening applications. The current sequence is that of a human soft tissue sarcoma-upregulated DNA of the invention. The current sequence is not shown within the specification per se but was submitted in CD format by the inventor.
                                                                                                                                                                                                                                                                                                                                                                                                                                               and
                                                                                                                                                                                                                                                                                                                                                 The invention relates to a novel method for detecting soft tissue sarcoma which comprises obtaining a first soft tissue sample from an individual
                                                                                                                                                                                                                                                                                                                                                                                                  Example 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Early detection of soft tissue sarcoma comprises determining expression of a gene in a first soft tissue sample and a normal soft tissue sample
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Aziz N,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    soft tissue sarcoma; cytostatic; gene therapy; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human soft tissue sarcoma-upregulated DNA - SEQ ID 7447.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADQ24627
                                                                                                            No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                            comparing the gene expression, also useful in treating soft tissue
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                                                             diagnostic and therapeutic polynucleotide; dithp; antiarteriosclerotic; antiinflammatory; cerebroprotective; antilipaemic; antidiabetic; immunosuppressive; neuroprotective; nootropic; neuroleptic; tranquilize; osteopathic; antiarthritic; antirheumatic; cytostatic; hepatotropic;
thrombolytic; anticoagulant; anorectic; vasotropic; antiulcer; gene therapy; protein replacement therapy; human; gene; ds.
                                virucide; haemostatic; anti-HIV; antithyroid; thyromimetic;
dermatological; antibacterial; fungicide; antiparasitic; an
                                                                                                                                           Human diagnostic and therapeutic polynucleotide (dithp), SEQ ID No 100.
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                                anticonvulsant;
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Homo sapiens.

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cc antidiabetic, immunosuppressive, neuroprotective, antilipaemic, cc antidiabetic, immunosuppressive, neuroprotective, notropic, neuroleptic, ctranquilizer, osteopathic, antiarthritic, antirheumatic, cytostatic, cc tranquilizer, osteopathic, antiarthritic, antirheumatic, cytostatic, cc dermatological, antibacterial, fungicide, antithyroid, thyromimetic, cc dermatological, antibacterial, fungicide, antiparasitic, anticonvulsant, cc dermatological, antibacterial, fungicide, antiparasitic, anticonvulsant, cc dermatologicical, antibacterial, fungicide, antiparasitic, anticonvulsant, cc dermatologicical, antibacterial, fungicide, antiparasitic, anticonvulsant, cc dermatologicical, antibacterial, for disagnosing, cascitopic, and antiulcer. The cc polypeptides are useful for diagnosing, preventing or treating diseases convers in cancer in cancer, cervix cancer, cancer, lung cancer, breast cancer, cervix cancer, bone cancer, lung cancer, breast cancer, cervix cancer, bone cancer, lung cancer, or other cell proliferative disorders (e.g. arteriosclerosis, cirhosis, hepatitis, polycythemia vera, primary cthrombocytopenia), autoimmune/inflammatory disorders (e.g. arteriosclerosis, cirhosis, hepatitis, polycythemia vera, primary chashimoto's thyroiditis, multiple sclerosis, osteoarthritis, rheumatoid carthritis, scleroderma, systemic lupus erythematosus), infections (e.g. cushing's syndrome or epilepsy), endocrine disorders (e.g. thrombosis, hypoglituitarism, hypogloralism, gigantism, goiter) metabolic disorders (e.g. thrombosis, hypoglituitarism, hypogloral disorders (e.g. ischaemic cerebrovascular disease, stroke, Alzheimer's disease, pick's disease, cancerbrotive tissue disorders (e.g. schaemic, or connective tissue disorders (e.g. schaemic), or consective disorders (e.g. schaemic), or consective disorders (e.g. schaemic), or consective disorders (e.g. schaemic), or consective d
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New human diagnostic and therapeutic polynucleotides and polypeptides, useful for diagnosing, treating or preventing e.g. leukemia, brain cancer, atherosclerosis, AIDS, thyroiditis, infections, obesity, stroke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jones AL, Dahl CR, Giel
Yu JY, Tuason O, Yap Pl
Peralta CH, Lewis SA, (
Kristnam SR, Kolluru V,
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17-JAN-2002; 2002US-0349413P.
17-JAN-2002; 2002US-0349946P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a novel isolated human diagnostic and therapeutic polynucleotide (designated dithp). The novel dithp polynucleotide comprises: any of 188 DNA sequences consisting of base pairs fully defined in the specification; a polynucleotide
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P-PSDB; ADE31156.
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Lason O, Yap PE, Amshey SR, Dam TC, Liu TF, Gerstin EH;
L, Lewis SA, Chen A, Marwaha R, Lan RY, Urashka ME;
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Sequence 3358 BP; 1105 A; 577 C; 601 G; 1075 T; 0 U; 0 Other,

Alignment Scores:

2110) CCTTTGCATCTTTTCGTTTCACAGTATTTAATTTTATGACTCTAAAAAATATGTTTCTTT	2169	밁
54	Leu	54	ঠ
2170) GTATAGCATGTTTTATTCATTCAGGGGTTTTTTGTTTTG	2229	뫄
53		53	ð
2230) ATCATAAGGAACAGGGTTGTCTGCTTACCTGAATATCAGCTATAGTCTATATTTGCCAAA	2289	D
53		53	र्
2290) CCAACCAATAGAAGAGCAAACATAGACAGGGGCAGTGATTGGCCTCTTATTGTTCGGGTC	2349	문
53		53	ર્ક
2350	ACAAGTTCTTATTATTGACGTTCATCATTAAGCAGTTATTGTCAACTTCAAGCCCATTTT	2409	말
53		53	ð
2410) ATAGGAAACTACAACAACGACACGTGCTTCCCACAGTGAAATAATAGGAAGTATAGG	2469	₽
53		53	ð
2470	CAGACAGGGTCCCCCCGCACCCCCTTTGTTTTAGAATACTACAGAGGCTACTGCCATAT	2529	뫄
53		. 53	ঠ
2530	TTAACATAAGGACATTAAAGATGCAATGCACAGAATTAAATCACACAATTACTTAC	2589	밁
53		53	ঠ
2590) AGAACGTGCTTCGTAAACTAACATACTGCAAAAAAGGTAAAATAAGAGAATATATAT	2649	문
53		53	S
2650) CATAAAGGCTGAAATAGTTTGCAGATACAGTTATGTATTTTGCCAAATAATGTATGT	2709	문
53		53	S
2710	GTACACGAATTTATAATTCTTAGCCTTTCTTAATAAAATGGTAAGAGGTTCATATCTGTA	2769	닭
53		53	ફ
2770	TTTTATCTTAGTAAACTGAACACAAAATTCACATATGGTGAGAAAAAATAGAAAGCAGTA	2829	망
53		53	S
2830	TGTCCATTTCAACTAAGTAGCAATAGATGTGCTACCACCATTCACCTAAATATTTCTGAA	2889	문
53		53	S
2890	CCAGGTG	2949	밁
53	ProGly	50	S
49 2950	LeuAlaLeuValGlnGlyValSerAspPheLeuLeuLeuGlyLysSerLeuAspIleAla 	3008	유 성
29 3009	LeuThr	10 3067	음 성
	-2_COPY_148_414 (1-267) x ADE31345 (1-3358)	-10-649-273	Sn
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                                                                                                                                                                                                                                                                             Murine; mouse; protease; calcium activated neutral protease type 5; CAPN5; tryptase 4; sialoglycoprotease; enzyme; genetic disease; neurological; neuropsychological; psychotic illness; transgenic animal; gene; ds.
06-DEC-2000; 2000US-0251803P
06-DEC-2000; 2000US-0251820P
                                                                           05-DEC-2001; 2001WO-US046405
                                                                                                                                                                             WO200245491-A2
                                                                                                                                                                                                                         Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                    Murine sialoglycoprotease-like gene sequence SEQ ID NO:7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-NOV-2002
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Alignment Scores: Pred. No.:

Query Match: Best Local Percent Similarity:

Similarity:

2.67e-101 983.00 84.21% 78.95% 70.97%

Length: Matches: Conservative: Mismatches:

Indels: Gaps:

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GluLysGluGluGlyIleGluLysGlyGlnIleLeuSerSerAlaAlaAspIleAlaAla

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AsnCysAspPheSerPheThrGlyLeuGlnHisValThrAspLysIleIleMetLysLys 120

TTGGCCAAAGACGGAAATAGATTCCATTTTACTATCAATCCACTATGCAGAATGCTAAG LeuAlaLysGlnGlyAsnArgPheHisPheAspIleLysProProLeuHisHisAlaLys 100

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LeuSerLeuIleLysHisProGluCysSerThrMetSerGlyGlyLysAlaIleGluHis 80

CTTTCTTTAATCAAACATCCAGAATGTTCTACAATGAGTGGTGGAAAAGCTATAGAACAG

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LeuLeuGlyLysSerLeuAspIleAlaProGlyAspMetLeuAspLysValAlaArgArg

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CTCCTTGGGAAGTCTTTGGACATAGCACCAGGCGACATGCTTGACAAGGTGGCAAGAAGA

LeuLeuIleSerGlyGlyHisCysLeuLeuAlaLeuValGlnGlyValSerAspPheLeu

CTTTTGATTTCTGGCGGYCACTGCCTGTTGGMRTTAGTCCAAGGTGTTTCCGATTTCCTG

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US-10-649-273-2_COPY_148_414 (1-267) x ABQ75508 (1-1572)

1 MetGluAlaHisAlaLeuThrIleArgLeuThrAsnLysValGluPheProPheLeuVal 20

ATGGAGGCTCACGCACTGACTATTAGGCTCACCAATAAAGTAGATTN-CCTTTTTTAGTT

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The present invention describes a non-human transgenic animal (I) comprising a disruption in a protease target gene (PG) selected from CC calcium activated neutral protease type 5 (CAPN5) gene, tryptase 4 gene (C and sialoglycoprotease-like gene. Also described is a targeting construct (II), comprising a first polynucleotide sequence homologous to at least a CC first portion of PG, a second polynucleotide sequence homologous to at CC least a second portion of PG and a selectable marker: (II) is useful for CC producing a transgenic mouse comprising a disruption in a protease target GC gene, by introducing (II) into a cell, introducing the cell into a CC blastocyst, implanting the resulting blastocyst into a pseudopregnant CC mouse, where the pseudopregnant mouse gives birth to a chimeric mouse, CC and breeding the chimeric mouse to produce the transgenic mouse. (I) is considered the crimeric mouse birth to a chimeric mouse, CC useful for identifying an agent that modulates the expression or function CC determining whether the expression or function of the disrupted protease target gene, by administering an agent to (I) and CC efficacy of proposed genetic and pharmacological therapies for human CC genetic diseases, such as neurological, neuropsychological or psychotic illness. The present sequence represents murine sialoglycoprotease-like gene sequence, which is used in an example from the present invention
Sequence 1572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel transgenic animal, comprising a disruption in protease target gene, is useful for identifying agents that ameliorates a phenotype associated with a disruption in a protease target gene.
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                                                                                         The invention relates to isolated polymucleotide (I) and polymentide (II) sequences. (I) is useful as hybridisation probes, polymerase chain
                                                                                                                                                                                                                                                     New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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23-AUG-2000; 2000US-00649167
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medical imaging; diagnostic;
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sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also use in diagnostics as expressed sequence tags for identifying expressed

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standard; DNA;

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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2734 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene potential; multi-lineage; cell commitment; haematopoietic stem cell; HSC; multipotent progenitor; MPP; common lymphoid progenitor; CLP; common myeloid progenitor; CMP; bone marrow stem cell; mouse; murine; ds.
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                                                               develop a gene expression map, in order to determine the discrete sub-
population where it is expressed. The present invention describes methods
for predicting the lineage commitment of genes associated with the self-
renewing haematopoietic (blood) stem cells (HSCs), as well as the non-
self renewing multipotent progenitors (MPPB), common lymphoid progenitors
(CLPB) and common myeloid progenitors (CMPB), which are collectively
referred to as bone marrow stem cells populations. As such, these methods
can be used to identify associated multi-lineage affiliated genes and
hence the underlying molecular mechanisms in physiological haematopoietic
development. This polynucleotide sequence is DNA associated with a murine
MPP sub population of cells of the invention.
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Search co	Дb	8	В	Qy	Дb	ş	DЪ	Ş	DЬ	Ş	Db	<i>Q</i>	망	Q	US-10-64	DB:
Search completed: June 16, 2005, 20:15:08 Job time : 396.989 secs	362 GCCATAAAA 370	257 SerIleLys 259	302 ATCCNNTATGNACCAAAATNTCNTNTTGGAGTAGACATNTCCAGAGAAGTTGCAGAAGCT 361	237 IleArgTyrGluProLysCysProLeuGlyValAspIleSerLysGluValGlyGluAla 256	242 GCATGGAATGGAATTGAANGATTACGTGCNGNCTTNGGCNTTNTACNTGANNTAGAAGAC 301	217 AlaTrpAsnGlyIleGluArgLeuArgAlaGlyLeuGlyIleLeuHisAspIleGluGly 236	182 ACGCAGTGCACGTTGTTGTGTCCACCTCCAAGACTGTGCACTGACAATGGCATCATGATT 241	197 ThrGlnCysThrLeuLeuCysProProProArgLeuCysThrAspAsnGlyIleMetIle 216	122 TCTGGAGGTGTTGCAAGTAACTTGTACATCCGAAAAGCATTGGAAAATTGTCGCAAATGCA 181	AlaLeuGluIl	62 GCTATTCTGTTTTGCAGCAGAGAAATTTGCTCTCTCCAGCTAACGCAGTATTAGTTGTA 121	157 AlaIleLeuPheCysLysGlnArgAspLeuLeuProGlnAsnAsnAlaValLeuValAla 176	2 GACATTGCTGCGGTACAGCATGCAACAGCGTGCCACCTTGCGAAAAGAACACATCGC 61	137 AspIleAlaAlaThrValGlnHisThrMetAlaCysHisLeuValLysArgThrHisArg 156	US-10-649-273-2_COPY_148_414 (1-267) x ADL86726 (1-371)	12 Gaps: 0

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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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-LOOPEXT=0 -UNITS=55tts_START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
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US-10-067-443-20
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ALIGNMENTS

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US-09-774-528-177
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US-09-774-528-177
                                                                                                  NUMBER OF SEQ ID NOS: 441
SOFTWARE: pt_FL_genes Version 2.0
SEQ ID NO 177
                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 177, Application US/09774528
Patent No. 6743619
                                                                                                                                                                             APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6743619el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
                                                                                                                                                                                                                                         APPLICANT:
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                                                                                                                                           FILE REFERENCE: 802
CURRENT APPLICATION NUMBER: US/09/774,528
CURRENT FILING DATE: 2001-01-30
               FEATURE:
NAMR/KEY: CDS
LOCATION: (205
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                                                        TYPE: DNA
ORGANISM: Homo
                                                                                     LENGTH: 1416
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Wang, Jian-Rui
Wang, Dunrui
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Zhao, Qing A.
Yang, Yonghong
Xue, Aidong J.
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Asundi, Vinod
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Alignment Scores:

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Best Local Similarity:
Sequence 23, Application US/10067443
Patent No. 6642041
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING
TITLE OF INVENTION: SPINAL CORD, MP-1
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              EXPRESSED
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CURRENT APPLICATION NUMBER: US/10/067,443
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: US 60/266,518
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: US 60/282,814
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 23
; LENGTH: 1526
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-067-443-23
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Best Local Similarity:
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                                                                                                AlaSerAsnPheTyrIleArgArgAlaLeuGluIleLeuThrAsnAlaThrGlnCysThr
                                                                                                                                                                                                                            LeuAlaLysGlnGlyAsnArgPheHisPheAspIleLysProProLeuHisHisAlaLys
                                                                                                                                                                                                                                                                                                                                                                                                               LeuLeuGlyLysSerLeuAspIleAlaProGlyAspMetLeuAspLysValAlaArgArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                        LeuLeuIleSerGlyGlyHisCysLeuLeuAlaLeuValGlnGlyValSerAspPheLeu
                         IleGluArgLeuArgAlaGlyLeuGlyIleLeuHisAspIleGluGlyIleArgTyrGlu
                                                      ThrValGlnHisThrMetAlaCysHisLeuValLysArgThrHisArgAlaIleLeuPhe
                                                                                                                                                                                                                                                                       ASTCYSASPPHeSerPHeThrGlyLeuGlnHisValThrASpLySIleIleMetLySLyS
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                                                                                                                                           TGTAAGCAGAGAGACTTGTTACCTCAAAATAATGCAGTACTGGTTGCATCTGGTGGTGTC
                                                                                                                                                      CysLysGlnArgAspLeuLeuProGlnAsnAsnAlaValLeuValAlaSerGlyGlyVal
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Matches:
Conservative:
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Indels:
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TITLE OF INVENTION: POLYNUCLECTIDE ENCODING A NOVEL METALOPROTEASE HIGHLY EXPRESSED
TITLE OF INVENTION: SPINAL CORD, MP-1
FILE REFERENCE: D0073 NP
CURRENT FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US/0/067,443
CURRENT FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SOFTWARE: PATENTIN Version 3.0
SEQ ID NO 1
LENGTH: 2197
TYPE: NAME: PATENTIN VERSION 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application Patent No. 6642041
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NAME/KEY: CDS
LOCATION: (231)..(1472)
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ThrValGlnHisThrMetAlaCysHisLeuValLysArgThrHisArgAlaIleLeuPhe
                                       GluLysGluGluGlyIleGluLysGlyGlnIleLeuSerSerAlaAlaAspIleAlaAla 140
                                                                                              AsnCysAspPheSerPheThrGlyLeuGlnHisValThrAspLysIleIleMetLysLys 120
                                                                                                                                                                                           CTTTCTTTAATAAAACATCCAGAGTGCTCCACCATGAGTGGTGGGAAAGCCATAGAACAT
                                                                                                                                                                                                        LeuSerLeuIleLysHisProGluCysSerThrMetSerGlyGlyLysAlaIleGluHis
                                                                                                                                                                                                                                               CTTCTTGGAAAGTCTTTGGACATAGCACCAGGTGACATGCTTGACAAGGTGGCAAGAAGA
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US-10-649-273-2_COPY_148_414 (1-267) x US-10-067-443-21 (1-1387)
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Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: homo
US-10-067-443-21
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US-10-067-443-21
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APPLICANT: Bristol-Myers Squibb Company
ITTLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE HIGHLY EXPRESSED
TITLE OF INVENTION: SPINAL CORD, MP-1
FILE REFERENCE: D0073 NP
CURRENT PILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
PRIOR PILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SOFTWARE: PatentIn version 3.0
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Patent No. 6642041
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                                                                                                                           MetGluAlaHisAlaLeuThrIleArgLeuThrAsnLysValGluPheProPheLeuVal 20
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                                         I.e.U.Le.U.C.L.VI.VeSerLe.u.AsplleAlaProGlyAspMetLeu.AspLyoValAlaArgArg
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LeuSerLeuIleLysHisProGluCysSerThrMetSerGlyGlyLysAlaIleGluHis
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Qy 58		Pred. No.: 1.34e-99 Length: 14364 Score: 824.50 Matches: 240	So Pi
Db 11744 TTTTGTTTTGTTAGTAATTTTCAATTTATTTCCTTTGCATCTTTTCGTTTCACAGTATTT 11803		C +C CC *** L CC	٥ (۵
Qy 57 57			;; `
Db 11684 TGAATATCAGCTATAGTCTATATTTGCCAAAGTATAGCATGTTTTATTCATTC		E SOL	
Qy 57 57		PatentIn ver	
Db 11624 GGGCAGTGATTGGCCTCTTATTGTTCGGGTCATCATAAGGAACAGGGTTGTCTGCTTACC 11683		FILING DATE: 2001-04-10	
Qy 57 57		FILING DATE: 2001-02-09 ADDITION NUMBER: 118	
Db 11564 AAGCAGTTATTGTCAACTTCAAGCCCATTTTCCAACCAATAGAAGAGCAAACATAGACAG 11623		CURRENT FILING DATE: 2002-02-05 PRIOR APPLICATION NUMBER 11S 60/266 518	
Qy 57 57		FILE REPERENCE: D0073 NP CURRENT APPLICATION NUMBER: US/10/067 443	
Db 11504 CTTCCCACAGTGAAATAATAGGAAGTATAGGACAAGTTCTTATTATTGACGTTCATCATT 11563	EXPRESSED I	TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE HIGHLY EXPRI- TITLE OF INVENTION: SPINAL CORD. MP-1	
Qy 57 57		GENERAL NO. 1074071 GENERAL TOWN. Dei 107401 M. Commission Commiss	
Db 11444 AATACTACAGAGGCTACTGCCATATATAGGAAAACAAACA		40	· • ·
Qy 57 57		RESULT 5	RE
Db 11384 TTAAATCACACAATTACTTACACCACAGACAGGGTCCCCCCCC		1305	Dp.
Qy 57 57		y 256 AlaSerIleLysValProGlnLeuLysMetGluIle 267	γQ
Db 11324 GGTAAAATAAGAGAATATATATAGATTAACATAAGGACATTAAAGATGCAATGCACAGAA 11383		1245	ф
Qy 57 57		y 236 GlyIleArgTyrGluProLysCysProLeuGlyValAspIleSerLysGluValGlyGlu 255	δ
Db 11264 TATTTTGCCAAATAATGTATGTGAAAGAACGTGCTTCGTAAACTAACATACTGCAAAAAA 11323		1185 ATTGCATGGAATGGTATTGAAA	ďα
Qy 57 57		y 216 IleAlaTrpAsnGlyIleGluArgLeuArgAlaGlyLeuGlyIleLeuHisAspIleGlu 235	γQ
Db 11204 AAATGGTAAGAGGTTCATATCTGTACATAAAGGCTGAAATAGTTTGCAGATACAGTTATG 11263		1125 GCAACACAGT	dg dg
Qy 57 57		y 196 AlaThrGlnCysThrLeuLeuCysProProProArgLeuCysThrAspAsnGlyIleMet 215	γo
Db 11144 ATGGTGAGAAAAAATAGAAAGAGTAGTACACAATTTTATAATTCTTAGCCTTTCTTAATA 11203		1065	ДĎ
Qy 57 57		y 176 AlaSerGlyGlyValAlaSerAsnPheTyrIleArgArgAlaLeuGluIleLeuThrAsn 195	δ
Db 11084 TACCACCATTCACCTAAATATTTCTGAATTTTATCTTAGTAAACTGAAAAAAATTCACAT 11143		1005	ф
Qy 57 57		y 156 ArgAlaIleLeuPheCysLysGlnArgAspLeuLeuProGlnAsnAsnAlaValLeuVal 175	δð
Db 11024 TTAATTTCTCCATTCTTTTTTGTTATGTTGTCCATTTCAACTAAGTAGCAATAGATGTGC 11083		945 GC	ДD
Qy 57 57		y 136 AlaAspIleAlaAlaThrValGlnHisThrMetAlaCysHisLeuValLysArgThrHis 155	Ş Ş
Qy 41 LeuLeuGlyLysSerLeuAspIleAlaProGlyAspMetLeuAspLysVal 57		y 127	B &
Db 10905 CTTTTGATTTCTGGAGGTCACTGTCTGTTGGCATTAGTTCAAGGAGTTTCAGATTTTCTG 10964		825 GAAAAGAGGTATATTTCTAATTAGTAAAGTTGAACAGATAAATATTCCTGGATTG 884	dg dg
Qy 21 LeuLeuIleSerGlyGlyHisCysLeuLeuAlaLeuValGlnGlyValSerAspPheLeu 40		y 121 GluLysGluGlyIle 126	8
Qy 1 MetGluAlaHisAlaLeuThrIleArgLeuThrAsnLysValGluPheProPheLeuVal 20		y 101 AsnCysAspPheSerPheThrGlyLeuGlnHisValThrAspLysIleIleMetLysLys 120 	dd VQ
US-10-649-273-2_COPY_148_414 (1-267) x US-10-067-443-20 (1-14364)		D 705 TTGGCCAAACAAGGAAATAGATTTCATTTTGACATCAAACCTCCCTTGCATCATGCTAAA 764	фa
/ Match: 59.53%		81 LeualaLysGlnGlyAsnArgPheHisPheAspIleLysProProBuHisHisAlaLys	Q ¦
Conservative:	_	b 645 CTTTCTTTPAATAAACATTCCACATCACCTCACATCACTCCCAAACCCATTACCTCACATCACTCCACATCACTCACATCACATCACTCACATCACTCACATCACTCACATCACTCACATCACTCACATCACTCACATCACTCACATCACTCACATCACTCACATCAT	밁

Query Match:	12943	.2884 GTTATGTAGTAAAATGCACAAAATAATAAAAATTTCAGGGTCTAAAAATAGTGTACTATGA	Db 12
Percent Similarity:	174	174	Ş.
Pred. No.:	12883	2824 TAAATGGTAGTAATTCATAGATGGAATTTTACATGGATATCAAAGAATAATTTTTTCAGA	Db 12
Alignment Scores:	174	174	Ş
; PUBLICATION INFORM US-09-596-002-38	12823	.2764 GTTTAACTGTATCTTAAACTTTATTCATTTAAAAATTATAAACTAAAGTGGGAAAATGTT	Db 12
; NAME/KEY: misc_fe	174	174	Ş
ORGANISM: M. cata	12763	2704 CACTATATTGTACCAGCCAAAATCCCTTTAATTGTGCTTAAAAGCCTTGACAAACATCCT	Db 12
	174	174	Qy
ر ا ا	12703	2644 AGCAGTGGGAGGTGGTATTCCAACTTTCGTGACACTAATGTTGATAAAGTTCTGATAATC	Db 12
; PRIOR FILING DATE:	174	174	Qγ
; CURRENT FILING DATE	12643	.2584 CCTTCATCCTTTGATGAAATCCCTTTGTTTGTTTGTTTTTTTAATAAGCCAGTCAAATTT	Db 12
; FILE REFERENCE: PI	174	174	Qy
a	12583	.2524 ACAATAAAGAAAGTAAATGCAGTAACTGCTATCACTATTTTTAGAAAAATAGGTGGATTT	Db 12
; APPLICANT: Lac	174	174	δ.
; Patent No. 6632636 ; GENERAL INFORMATION	12523	12464 TAGCTTCTATGGCACATAAGTCTAATTTTGCATCTTCTTGTTGGATTTAAAAGAGGGCTT	Db 12
US-09-596-002-38 ; Sequence 38, Applica	174	174	γ
SULT 6	12463	2404 GATAGGAAAGACTAACAGCCATTTCTTGTACTAGTTTGGTAGCTTTATGGGACAGCTGTA	Db 12
13484 (174	174	8
226	12403	12344 TGTTTAGGÄTGAACAGATCTTTATGCCTTATGCTAGCCCTGACAGTATGAAATTATGCAG	Db 12
13	174	174	
219	12343	12284 ATTTTATAGTAATAGTTACACTTTGCAATATGTTACTTTTTTCCCAAGACCTTGACCTTG	Db 12
13	174	174	δ
Оу 218	12283	12224 GTTTTGTÄÄGCAGÄGAGACTTGTTÄCCTCAAAATAATGCAGTACTGGTÄÄGTTTTÄTCTC	Db 12
13304	174		Ş
Qy 207 giệuCys	12223	12164 TGCCACAGTACAGCACACAATGGCATGTCATCTTGTGAAAAGAACACATCGGGCTATTCT	Db 12
13244	159	139 aAlaThrValGlnHisThrMetAlaCysHisLeuValLysArgThrHisArgAlaIleLe	Ş
187	12163		Db 12
H.	139	125GlyIleGluLysGlyGlnIleLeuSerSerAlaAlaAspIleAl	δ
175	12103	12044 GGTATATTTCTAATTAGTAAAGTTGAACAGATAAATATTCCTGGATTGTGCCTAAAAATA	Db 12
13	124	124	δ
Оу 174	12043	11984 TCTTTTÄCTGGACTTCAACACGTTACTGATAAAATAATAATGAAAAAGGAAAAAGAGGAA	Db 11
Db 13064 ATAGATA:	124		
Qy 174	11983		Db 11
13	104	GlyAsnArgPheHisPheAspIleLysProProLeuHisHisAlaLysAsnCysAspPhe	
Qy 174	11923		Db 11:
12	84		ş
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	Length: 94750 Matches: 87 Conservative: 40 Mismatches: 101 Indels: 29	28 ten Mat Con Mis	3,21e- 308.50 49.61% 33.98% 22.27%	cores: llarity: Similarity:	nent So No.: nt Simi Local S	Alignm Pred. Score: Percen Best I Query
	No. 6632636 38	template ID		M. cat misc_f RMATIO INFOR 38	ORGANI FEATUR FEATUR NAME/K OTHER UBLICA 9-596-	US-0
			FLOGLA	38 94750	OFIWARE: Q ID NO LENGTH:	 SB o
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æ	ICES OF MORAXELLA CATARRHALIS GENOME	SEQUEN 09/596,	NUCLE 0008-4 00MBER NUMBER	OI I	TITLE OF INVENT FILE REFERENCE: CURRENT APPLICA CURRENT FILING	
		Robert, E. handra	= ,	INFORMATION: INFORMATION: ANT: Lagace ANT: Patterson,	GENERAL INFO APPLICANT: APPLICANT: APPLICANT:	
		US/09596002	ion	002-38 38, Applicat	6 596-(RESULT US-09-
	AAGGCATCCGCTATGAACCAAAG 13533	TAGET THE CATTER CATTER CATTAGE AND A TREE TO THE TREE TO THE TR	TTGGGCATTTT	CTGGCTTG	13484	용 원
13483	TTATTTAGGAATGGTATTGAAAGA	ATTTAATGCT	TTGATTTT.	TGGAGCTA	N	В
226	>				219	Ś
13423	CATAACTATGTAAATATTAATTGCCATTTTATCATACTAAGCCTTCTTCCTTC	ATTAATTGCCA'	ATGTAAAT	TCATAACT	13364	В
218			1 1 1 1 1 1 1	!	218	Ś
13363	 GCATGGTAAGCCACAGGATATACGTGCTTCA	ATTATGAT	CTGATAATGGC	ATGCA	0 0	ß ?
218	eAlaTro	3]vīleMetīl	rasnasni	Tevolle	2	₹
207	aThrGlnCysThrLeuLeuCysProProProAr 	ArgAlaLeuGluIleLeuThrAsnAlaThrGln 	euGluIle GGAAATT	gArgAlaLe	187 13244	음 성
13243	TIGGTTTTCTCAATTCCTTCAGGTTGCATCTGGTGGTGTCGCAAGTAACTTCTATATCCG	 	CTCAATTC	TTGGTTTT	13184	рb
187	ValAlaSerGlyGlyValAlaSerAsnPheTyrIleAr	valal			175	ð.
13183	CTGATATTTTTCTCCAGGTTTAATTAGCAGCTTGGTTCATATCCATATATGATAGTTATT	GTTTAATTAG	TTCTCCA	CTGATATTT	13124	망
174		1			174	Ś
13123	atagatatgtcatctgcccattacccatctcaaaatgggatagtttattattgtttaatg	CCATTACCCA	STCATCTG	ATAGATATO	13064	망
174				1	174	Ś
13063	AGTAATGTTTGTATGCTATTAGAATTATTAGTAATTTTTTTT	TATTAGAATTA:	TGTATGC	AGTAATGTT	13004	₽
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13003	ttgaaattatatataaataatatttagatgaaaggttggaagaa	[AAATATTTAG]	TATTAAA	TTGAAATT!	12944	문
174					174	Ś

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; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 806
; LENGTH: 1053
; TYPE: DNA
; ORGANISM: M.catarrhalis
; US-09-540-236-806
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                                                                                                       Sequence 806, Application US/09540236
Patent No. 6673910
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILL REFERENCE: 2709.2005-001
CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT FILING DATE: 2000-04-04
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Percent Similarity:
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GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
                                                                                                                                       Sequence 884, Application Patent No. 6551795
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1999-02-18 MBER: US 60/074,788

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CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60,
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60,
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 884
LENGTH: 1059
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Query Match:
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 CAGCCGCGCTGGCCGATG 40
                               GluproLysCysproLeu 245
                                                                                               GlyIleGluArgLeuArgAlaGlyLeuGlyIleLeuHisAspIleGluGlyIleArgTyr 239
                                                                                                                                      CAGGTGTTCTACGCCCGCCCCCCCCCCCCCCCCCCACACCATGATCGCCGATGATCGCCTACGCC 109
                                                                                                                                                           ThrLeuLeuCysProProProArgLeuCysThrAspAsnGlyIleMetIleAlaTrpAsn 219
                                                                                                                                                                                                                                                                                                       PheCysLysGlnArgAspLeuLeuProGlnAsnAsnAlaValLeuValAlaSerGlyGly
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                                                                      GGCTGCCAGCGCCTGCTCGCCGGC--
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APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ITITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT FILING DATE: 1999-02-18
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 801
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ORGANISM: Pseudomonas
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                            ValAlaSerAsnPheTyrIleArgArgAlaLeuGluIleLeuThrAsnAlaThrGlnCys 199
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RESULT 10
US-09-557-884-1/c
; Sequence 1, Application US/09557884
; Patent No. 6506581
; GENERAL INFORMATION:
APPLICANT: Fleischmann et al.
TTTT:E OF INVENTION: The Nucleotide sequence of the Haemophilus influenzae Rd /
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                                                                                          US-10-649-273-2_COPY_148_414 (1-267) x US-09-557-884-1 (1-1830121)
                                                                                                                                      Query
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                        Match:
                                           552881
                                                                                                                                                                                                                                            TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ
                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: 301-309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/476,102
FILING DATE: JUN-5-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1168
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ThrLeuLeuCysProProProArgLeuCysThrAspAsnGlyIleMetIleAlaTrpAsn 219
                                         AIGGAAGGCATTIACITGCGCCAATGCTTGATGACAATTCACCGCACTTTCCTTTTGTT
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                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                               NAME: Michelle S. Marks
REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PB186P3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/557,884 FILING DATE: 25-Apr-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: 3 1/2 inch diskette
COMPUTER: Dell Pentium
OPERATING SYSTEM: MS DOS V6.22
SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: MD
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                                                                                                                                                                                                                                                                                                                                        TELEFAX: 301-309-8439
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Sequence 1, Application Patent No. 6528289 GENERAL INFORMATION:
                          ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: 3 1/2 inch diskette

COMPUTER: Dell Pentium

OPERATING SYSTEM: MS DOS v6.22

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/643,990A

FILING DATE: 23-Aug-2000

CLASSIFICATION: <Unknown>
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J. Craig Venter
Vention: The Nucleotide sequence of
the Haemophilus influenzae
The and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genom
STREET: 9410 Key West
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GlnCysThrLeuLeuCysProProArgLeuCysThrAspAsnGlyIleMetIleAla 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---ATTAAATGTAAG---
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Hamilton O. Smith
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SEQUENCE CHARACTERISTICS:
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FILING DATE: 1995-06-07
APPLICATION NUMBER: 08/426,787
PILING DATE: 1995-04-21
ATTORNEY, AGENT INFORMATION:
NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PB186P1C1
TELEPHONE: 301-610-5790
TELEPHONE: 301-610-5790
TELEPAX: 310-309-8439
552341 GGTGGCGAAGTGTTTTATĆCTCAAĆCTCAATTTTGTACAGATAATGGTGCGATGATTGCT 552282
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TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                         GCAATTAAAAACGAGGGCGAACTGATAGAGCAA-----
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                    GlnCysThrLeuLeuCysProProProArgLeuCysThrAspAsnGlyIleMetIleAla 217
                                                                                GGAGGGGTGAGCGCAAATAAAAAACTCCGAGAAACGCTTGCGCACTTAATGCAAAATTTA 552342
                                                                                               GlyGlyValAlaSerAsnPheTyrIleArgArgAlaLeuGluIleLeuThrAsnAlaThr 197
                                                                                                                                                           ---ATTAAATGTAAG---CGTGCATTGAAAGAAACAGGCTATAAACGTTTAGTGATTGCG 552402
                                                                                                                                                                                            IleLeuPheCysLysGlnArgAspLeuLeuProGlnAsnAsnAlaValLeuValAlaSer 177
                                                                                                                                                                                                                                          ATTIGCTTATGCTTTCCAAGATGCGGTGGTGGATACTCTTGCC------
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APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Serille Reference: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
UNUMBER OF SEQ ID NOS: 16825
SEQ ID NO 6612
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Best Local Similarity:
Query Match:
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; ORGANISM: Myxococcus xanthus
US-09-902-540-6612
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GENERAL INFORMATION:
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                                                                                                                                                                  IleIleMetLysLysGluLysGluGluGlyIleGluLysGlyGlnIleLeuSerSerAla 135
                                                                                                 AlaAspIleAlaAlaThrValGlnHisThrMetAlaCysHisLeuValLysArgThrHis 155
                                                                                                                                                                                                                            LeuHisHisAlaLysAspCysAspPheSerPheThrGlyLeuGlnHisValThrAspLys 115
                              ArgAlaIleLeuPheCysLysGlnArgAspLeuLeuProGlnAsnAsnAlaValLeuVal 175
                                                                  GCGGATTTGTGCGCGTCCTTCCAGGAGGCCGTGGCGGACGTGCTGTCGAAGAAG-----
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SEQ ID NO 503
LENGTH: 2582
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APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and PILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT APPLICATION NUMBER: 60/217,883
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR PILING DATE: 2000-07-10
PRIOR PILING DATE: 2000-07-10
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AlaAspIleAlaAlaThrValGlnHisThrMetAlaCysHisLeuValLysArgThrHis 155
                                         GCGGTGCTGCACCACGTGCAGAAGCACGGCGTGCCGCAGGGGCAGGCGCTG-----
                                                                                IleIleMetLysLysGluLysGluGluGlyIleGluLysGlyGlnIleLeuSerSerAla 135
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APPLICANT: GARY ERETON
APPLICANT: GARY ERETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILI
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR PILING DATE: 1999-04-09
PRIOR FILING DATE: 1999-04-09
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SEQ ID NO 2341
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TYPE: DNA
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US-08-087-797-1
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                                                                                                                                                             TELEFAX: 704 334 2014
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
MOLECULE TYPE:
HYPOTHETICAL: I
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                SOFTWARE: PATENTIN Release #1.0, 1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/087,797
FILING DATE: 14-JUL-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Pasteurella Haemolytica
TITLE OF INVENTION: Glycoprotease
TITLE OF INVENTION: Gene and the Purified Enzyme
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bell, Seltzer, Park & Gibson, P.A.
                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: 704 377 1561
TELEFAX: 704 334 2014
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MEDIUM TYPE: Floppy disk
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                                                                                                                                             SEQUENCE CHARACTERISTICS:
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                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                           REGISTRATION NUMBER: 22807
REFERENCE/DOCKET NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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STATE: No. 5543312th Carolina
                                                                 TOPOLOGY:
                                                                                                  TYPE: nucleic acid
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                                                                                                                                                                                                                                                                              Layton, Jr., Samuel G.
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Abdullah, Khalid M.
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Query Match:
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1080
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                                   GlyIleGluArgLeuArg
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                                                                                                                                                GTAAGTGCCAATAAACAATTACGAGCAGACCTTGCGGAAATGATGAAAAAATTAAAAGGC 1019
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Matches:
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Search completed: June 17, 2005, 02:16:07 Job time : 1068.63 secs

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-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=bitssum62
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-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
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-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WALT -DSPBLCCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Ygapop 10.0, X
Ygapop 6.0, X
Fgapop 6.0, X
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Published_Applications_NA: *
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17:
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/cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US09E_PUBCOMB.seq:*
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/cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
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/cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
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FILE REFERENCE: 802CON
CURRENT APPLICATION NUMBER: US/10/120,988
CURRENT FILING DATE: 2002-04-11
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PRIOR FILING DATE: 2001-01-30
NUMBER OF SEQ ID NOS: 441
SOFTWARE: pt_FL_genes Version 2.0
SEQ ID NO 177
LENGTH: 1416
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NAME/KEY: CDS
LOCATION: (205)..(1305)
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TYPE: DNA
ORGANISM: Homo sapiens
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ProLysCysProLeuGlyValAspIleSerLysGluValGlyGluAlaSerIleLysVal
                                                        IleGluArgLeuArgAlaGlyLeuGlyIleLeuHisAspIleGluGlyIleArgTyrGlu
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CURRENT FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 23, Application No. US20 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING
TITLE OF INVENTION: SPINAL CORD, MP-1
FILE REFERENCE: D0073 NP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH:
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                                          ThrValGlnHisThrMetAlaCysHisLeuValLysArgThrHisArgAlaIleLeuPhe
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; Sequence 23, Application US/10649273
; Publication No. US20040043407A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE, MP-1
FILE REFERENCE: D0073 CNT
; CURRENT APPLICATION NUMBER: US/10/649,273
; CURRENT FILING DATE: 2003-08-27
; PRIOR APPLICATION NUMBER: US 60/266,518
; PRIOR APPLICATION NUMBER: US 60/266,518
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; PRIOR APPLICATION NUMBER: US 60/266,518
; PRIOR APPLICATION NUMBER: US 60/266,518
; PRIOR APPLICATION NUMBER: US 60/262,814
; PRIOR FILING DATE: 2001-04-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn version 3.2; SEQ ID NO 23; LENGTH: 1526; TYPE: DNA; ORGANISM: homo sapiens US-10-649-273-23
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CURRENT FILING DATE: 2003-08-29
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 10/067,443
PRIOR FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SOFTWARE: PatentIn version 3.2
SEQ ID NO 23
LENGTH: 1526
                                           Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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Sequence 23, Application US/10651722
Publication No. US20040048302A1
GENERAL INFORMATION:
US-10-649-273-2_COPY_148_414 (1-267)
                                                                                                                             Score:
                                                                                                                                               Pred. No.:
                                                                                                                                                                Alignment Scores:
                                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: homo sapiens
US-10-651-722-23
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CURRENT APPLICATION NUMBER: US/10/651,722
CURRENT FILING DATE: 2003-08-29
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TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE, MP-1
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; Sequence 1, Application US/10067443
; Publication No. US20030082782A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL MET
; TITLE OF INVENTION: SPINAL CORD, MP-1
; FILE REFERENCE: DO073 NP
; CURRENT APPLICATION NUMBER: US/10/067,443
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: US 60/266,518
; PRIOR APPLICATION NUMBER: US 60/266,518
; PRIOR APPLICATION NUMBER: US 60/282,814
; PRIOR APPLICATION NUMBER: US 60/282,814
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.0
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LENGTH: 2197
TYPE: DNA
ORGANISM: HOMO
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NAME/KEY: CDS
LOCATION: (231)..(1472)
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Percent Similarity:
Best Local Similarity:
Query Match:
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Publication No. US20040043407A1

GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company

TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE, MP-1

FILE REFERENCE: D0073 CNT

CURRENT APPLICATION NUMBER: US/10/649,273

CURRENT FILING DATE: 2003-08-27

PRIOR APPLICAN NUMBER: US/10/649,273
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PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 10/067,443
PRIOR FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
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TYPE: DNA
ORGANISM: Homo:
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LOCATION: (231)..(1472)
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                                                         ACAGTACAGCACACAATGGCATGTCATCTTGTGAAAAGAACACATCGGGCTATTCTGTTT 115
                                                                            ThrValGlnHisThrMetAlaCysHisLeuValLysArgThrHisArgAlaIleLeuPhe 160
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APPLICANT: BISTOIL-Myers Squibb Company
FILE OF INVENTION: POLYNUCLEOTIDE ENCODING A P
FILE REFERENCE: D00773 DTV
CURRENT APPLICATION NUMBER: US/10/651,722
CURRENT FILING DATE: 2003-08-29
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
PRIOR FILING DATE: 2001-02-05
PRIOR FILING DATE: 2002-02-05
PRIOR FILING DATE: 2002-04-10
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SOFTWARE: PATENTIN VERSION 3.2
SEQ ID NO 1
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US-10-651-722-1
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NAME/KEY: CDS
LOCATION: (231
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ORGANISM: Homo
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                                                                                                                732 CITTIGATITICIGAGGICACIGICIGITGGCATTAGTITCAAGGAGTITCAGATTITCIG
61 LeuSerLeuIleLysHisProGluCysSerThrMetSerGlyGlyLysAlaIleGluHis
                                                                                                                                 21 LeuLeuIleSerGlyGlyHisCysLeuLeuAlaLeuValGlnGlyValSerAspPheLeu
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APPLICANT: WARRINAR, Anita; HAPALIA, MY:;
APPLICANT: TRAN, Bao; DUGGAN, Brendan M.;
APPLICANT: WARREN, Bridget A.; ISON, Craig H.;
APPLICANT: HONCHELL, Cynthia D.; MGUYEN, Danniel B.;
APPLICANT: LU, Dyung Aina M.; LEE, Ernestine A.;
APPLICANT: BARROSO, Ines; RAMKUWAR, Jayalaxmi;
APPLICANT: BARROSO, Ines; RAMKUWAR, Jayalaxmi;
APPLICANT: GRIFFIN, Jennifer A.; LI, Joana X.;
APPLICANT: GRIFFIN, Jennifer A.; LI, Joana X.;
APPLICANT: HONGHIN, Jennifer A.; LI, Joana X.;
APPLICANT: BAUGHN, Mariah R.; BOROWSKY, Mark L.;
APPLICANT: BAUGHN, Mariah R.; BOROWSKY, Mark L.;
APPLICANT: HASON, Partircia M.; GURURAJAN, Rajagopal;
APPLICANT: LEE, Sally; BECHA, Shanya D.;
APPLICANT: LEE, Soo Yeun; TRAN, Uyen K.;
APPLICANT: LEE, Soo Yeun; TRAN, Uyen K.;
APPLICANT: LU, Yan; ZEBARAJADIAN, Yeganeh
TITLE OF INVENTION: PROTEIN MODIFICATION AND MAINTENANCE
FILE REFERENCE: PF-1040 USN
CURRENT APPLICATION NUMBER: PCT/USO2/19360
PRIOR APPLICATION NUMBER: DCT/USO2/19360
PRIOR APPLICATION NUMBER: US 60/300,508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: GANDHI,
APPLICANT: SWARNAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 36, Application US/104 Publication No. US20050069877A1
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                                                                                                                                             MAINTENANCE MOLECULES
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PRIOR PILING DATE: 2001-07-06
PRIOR APPLICATION NUMBER: US 60/303,445
PRIOR APPLICATION NUMBER: US 60/305,405
PRIOR APPLICATION NUMBER: US 60/311,445
PRIOR FILING DATE: 2001-07-13
PRIOR PILING DATE: 2001-08-09
PRIOR PILING DATE: 2001-08-09
PRIOR PILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/314,821
PRIOR APPLICATION NUMBER: US 60/315,992
PRIOR APPLICATION NUMBER: US 60/378,205
PRIOR PILING DATE: 2001-08-29
PRIOR PILING DATE: 2002-05-03
NUMBER OF SEQ ID NOS: 56
SOFTWARE: PERL PROGram
SEQ ID NO 36
LENGTH: 2572
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                              AlaSerAsnPheTyrI1eArgArgAlaLeuGluIleLeuThrAsnAlaThrGlnCysThr
                                                                                                                       CysLysGlnArgAspLeuLeuProGlnAsnAsnAlaValLeuValAlaSerGlyGlyVal 180
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Best Local Similarity:
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; ORGANISM: homo
US-10-067-443-21
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APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE HIGHLY EXPRESSED
TITLE OF INVENTION: SPINAL CORD, MP-1
FILE REFERENCE: D0073 NP
CURRENT APPLICATION NUMBER: US/10/067,443
CURRENT FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 21
LENGTH: 1387.
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US-10-649-273-21
US-10-649-273-2_COPY_148_414 (1-267)
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                                                                                                                                                                                                             ; ORGANISM: homo US-10-649-273-21
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CURRENT FILING DATE: 2003-08-27
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 10/067,443
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
PRIOR FILING DATE: 2001-04-10
PRIOR FILING DATE: 2001-04-10
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Publication No. US20040043407A1
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                                                                                                                                                                                                                                                   TYPE: DNA
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Sequence 21, Application US/10651722
Phblication No. US20040048302A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
ITTLE OF INVENTION: POLYNUCLEOTIDE ENCODING A 1
FILE REFERENCE: D0073 DIV
CURRENT APPLICATION NUMBER: US/10/651,722
CURRENT FILING DATE: 2003-08-29
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 10/067,443
PRIOR FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/282,814
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; PRIOR FILING DATE: 2001-04-10; NUMBER OF SEQ ID NOS: 71; SOFTWARE: PATENTIN VERSION 3.2; SEQ ID NO 21; LENGTH: 1387; TYPE: DNA; ORGANISM: homo sapiens
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GlyIleArgTyrGluProLysCysProLeuGlyValAspIleSerLysGluValGlyGlu
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                                           AlaThrGlnCysThrLeuLeuCysProProProArgLeuCysThrAspAsnGlyIleMet
                                                                                                                                                      ArgAlaIleLeuPheCysLysGlnArgAspLeuLeuProGlnAsnAsnAlaValLeuVal 175
                                                                                                                                                                                                                                                                                     AlaAspIleAlaAlaThrValGlnHisThrMetAlaCysHisLeuValLysArgThrHis 155
                                                                                                                                                                                                                                                                                                                                                                                   GAAAAAGAGGAAGGTATATTTCTAATTAGTAAAGTTGAACAGATAAATATTCCTGGATTG
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Sequence 1047, Application US/10887553A

Publication No. US20050085436A1

GENERAL INFORMATION:
APPLICANT: Li, Hao
TITLE OF INVENTION: with insulin signalling dysregulation
TITLE OF INVENTION with insulin signalling dysregulation
FILE REFERENCE: 4-33262
CURRENT APPLICATION NUMBER: US/10/887,553A
CURRENT FILING DATE: 2004-07-08
PRIOR APPLICATION NUMBER: 60/485,883
PRIOR APPLICATION NUMBER: 60/485,883
SPRIOR FILING DATE: 2003-08-07
NUMBER OF SEQ ID NOS: 1208
SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 1047
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Best Local Similarity:
Query Match:
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; ORGANISM: human
US-10-887-553A-1047
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AlaAspIleAlaAlaThrValGlnHisThrMetAlaCysHisLeuValLysArgThrHis 155
                                                           TGCCTAAAAATAGCTGCTCATTTCTGCAGGTATGAGAAGGGGGCAAATCCTGTCTTCAGCA
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                                                                                                                                          GluLysGluGluGlyIle-----
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; LENGTH: 1245
; TYPE: DNA
; ORGANISM: Homo :
US-10-012-140-6
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APPLICANT: Kapeller-Libermann, Rosana
APPLICANT: Kapeller-Libermann, Rosana
APPLICANT: Glucksmann, Maria A.
TITLE OF INVENTION: 38650, 28472, 5495, 65507, 81588, AND
TITLE OF INVENTION: 14354 METHODS AND COMPOSITIONS OF HUM
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 38155204900
CURRENT APPLICATION NUMBER: US/10/012,140
CURRENT PILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: 60/246,772
PRIOR APPLICATION NUMBER: 60/246,772
PRIOR APPLICATION NUMBER: 60/246,772
PRIOR APPLICATION NUMBER: 60/249,185
PRIOR APPLICATION NUMBER: 60/249,185
PRIOR PILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: 60/249,185
PRIOR APPLICATION NUMBER: 60/249,185
PRIOR PILING DATE: 2000-11-15
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US-10-012-140-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 49
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APPLICANT: Leiby, Kevin R.
APPLICANT: Leiby, Kevin R.
APPLICANT: Kapeller-Libermann, Rosana
APPLICANT: Glucksmann, Maria A.
TITLE OF INVENTION: 38650, 28472, 5495, 6550
TITLE OF INVENTION: 14354 METHODS AND COMPO
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 381552004900
CURRENT APPLICATION NUMBER: US/10/012,140
CURRENT FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: 60/246,768
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: 60/246,772
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                                       NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 4
LENGTH: 1820
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              ORGANISM: Homo
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; LOCATION: (146)...(1390)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1820)
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US-10-012-140-4
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APPLICANT: NAGAHARI, KENJI

APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
FILE REFERENCE: 084335/0160
CURRENT APPLICATION NUMBER: US/10/094,749
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 60/350,435
PRIOR PILING DATE: 2002-01-24
PRIOR PILING DATE: 2002-01-24
PRIOR PILING DATE: 2001-09-14
PRIOR PILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 3381
SOFTWARE: PATENTIN VET. 2.1
SOFTWARE: PATENTIN VET. 2.1
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Best Local Similarity:
Query Match:
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US-10-094-749-400
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OTSUKI, TETSUJI
WAKAMATSU, AI
SATO, HIROYUKI
ISHIZUKO
YAMAMOTO, JUN-ICHI
ISONO, YUUKO
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NAGAI, KEIICHI
IRIE, RYOTARO
TAMECHIKA, ICHIRO
SEKI, NAOHIKO
YOSHIKAWA, TSUTOMU
OTSUKA, MOTOYUKI
AATTGTGATTTTTCCTTTTACTGGACTTCAACACGTTACTGATAAAAATAATGAAAAAG 1144
                  AsnCysAspPheSerPheThrGlyLeuGlnHisValThrAspLysIleIleMetLysLys 120
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            ProGlnLeuLysMetGluIle 267
                                                                       ProLysCysProLeuGlyValAspIleSerLysGluValGlyGluAlaSerIleLysVal 260
                                                           ---TGATGTCCTCTTGGAGTAGACATATCAAAAGAAGTTGGAGAAGCTTCCATAAAAGTA
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Search completed: June 17, Job time: 1824.86 secs 2005, 08:03:19

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Command line parameters:

-MODEL-frame+ p2n.model -DEV=xlp
-MODEL-frame+ p2n.model -DEV=xlp
-Q-/cgn2_1/USPTO_spool_p/US10649273/runat_15062005_111416_6030/app_query.fasta_1.1429
-DB=GenEmb1 -QFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS-bits -START=1 -END=-1 -MATRIX=blosum62 -FRANS=human40.cdi -LIST=45
-DCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFWT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER-US10649273_@CGN 1 1 7742 @runat 15062005_111416_6030 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQÜERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPEXT=0.5 -FGAPOP=6
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELDET=6 -DELEXT=7
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Listing first 45 summaries
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Perfect score:
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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ALIGNMENTS

Alignment Scores: pred. No.: Score: Score: Percent Similarity: Best Local Similarity: Query Match:	TITLE JOURNAL FEATURES SOURCE ORIGIN	SOURCE ORGANISM REFERENCE AUTHORS	N ON
ores: larity: imilarity:	Nucleic acir Patent: US (1. /ou /mc	Unknown. Unknown. Unclassified. 1 (bases 1 to 1416) 1 Tang,Y.T., Zhou,P., Zhang,J., Zhao,Q.A.,	AR541929 Sequence 177 from paten AR541929 AR541929.1 GI:53934009
2.24e-113 1240.00 100.00\$ 100.00\$ 100.00\$	Nucleic acids and polypeptides Patent: US 6743619-A 177 01-JUN-2004; Location/Qualifiers Location="unknown" /organism="unknown" /mol_type="genomic DNA"	Unknown. Unknown. Unclassified. 1 (bases 1 to 1416) 1 (bases 1, Zhou, P., Goodr. Zhang, Y.T., Zhoo, Q.A., Yang, Wang, D. and Drmanac. R.T.	ď
Length: Matches: Conservative: Mismatches: Indels:	tides D1-JUN-2004; ers wn" ic DNA"	Unknown. Unknown. Unclassified. 1 (bases 1 to 1416) 1 (bases 1, Kang, P., Goodrich, R., Liu, C., Asundi, V., Ren, F., Tang, Y.T., Zhou, P., Goodrich, R., Liu, C., Wehrman, T., Wang, JR., Wang, J., Zhang, J., Zhang, J., Xang, Y., Xue, A.J., Wehrman, T., Wang, JR., Wang, D. and Drmanac. R.T.	1416 bp DNA US 6743619.
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		Ren, F., Wang, JR.,	PAT 08-OCT-2004

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REFERENCE
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                                                   Chen, J., Feder, J.N., Nelson, T.C., Krystek, S.R. and Polynucleotides encoding a novel metalloprotease, M Patent: US 6642041-A 23 04-NOV-2003; Location/Qualifiers
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Chen, J., Feder, J.N.,
                                                                                                    Unclassified.
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                                                                                               BC011904 1908 bp mRNA linear Homo sapiens O-sialoglycoprotein endopeptidase-like clone MGC:20293 IMAGE:4121450), complete cds. BC011904 BC011904 GI:40225818
Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1908)

Strausberg,R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Klausner,R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
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Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Haghighi,P.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
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DNA Sequencing by: National Institutes of Health Intramura
Sequencing Center (NISC),
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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On Dec 19, 2003 this sequence version replaced gi:15080281
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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DEFINITION

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MSGGKALEHLAKQGNRFHFDIKFPLHHAKNCDFSFTGLQHVTDKIIMKKEKEGIEKG
QILSSAADIAATVQHTWACHLVKRTHHAILFCKQRDLLPQNNAVLVASGGVASNFYIR
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1 (Dases I to 1387)
Chen, J., Feder, J.N., Nelson, T.C., Krystek, S.R. and Duclos, Polynucleotides encoding a novel metalloprotease, MP-1
Polynucleotides encoding a novel metalloprotease, MP-1
Polynucleotides encoding a novel metalloprotease, MP-1
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ProProProArgLeuCysThrAspAsnGlyIleMetIleAlaTrpAsnGlyIleGluArg
                                                                       ArgAspLeuLeuProGlnAsnAsnAlaValLeuValAlaSerGlyGlyValAlaSerAsn
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                                              US-10-649-273-2_COPY_176_414 (1-239) x HSA295148 (1-1387)
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Homo sapiens Eukarver
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AJ295148
AJ295148.1 G
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Cloning and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chen, J.M.
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Unpublished
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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LeuLeuAlaLeuValGlnGlyValSerAspPheLeuLeuLeuGlyLysSerLeuAspIle
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coning and sequencing of a second human putative
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VEFFFLVLLISGGHCLLALVQGVSDFILLGKSLDIAFGDMLDKVARRLSLIKHPECST
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SKVEQINIPGLICLKIAHFCRYEKGQILSSAADIAATVQHTMACHLVKRTHRAILFCK
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/db_xref="GI:11071727"
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Sequence 6 from AX664697
                        of human proteins and uses thereof Patent: WO 02074960-A 6 26-5EP-2002; Millennium Pharmaceuticals, Inc. (US)
                                                                                      Leiby, K.R., Ka
38650, 28472,
                                                                                                                                                    Bukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Butheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                              Homo sapiens
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                                                                                    Kapeller-Libermann,R. and Glucksmann,M. 2, 5495, 65507, 81588 and 14354 methods
                                                                                                                                                                                                                                                                  GI:29164457
                                                                                                                                                                                                                                                                                                        Patent W002074960.
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                                                                                          14354 methods and
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/organism="Homo sapiens"

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RESULT 8
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                           Homo sapiens (human)
                                                                    AX664695.1
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                                                                                                                                                       IleSerLysGluValGlyGluAlaSerIleLysValProGlnLeuLysMetGluIle 239
                                                                                                                                                                                                                      GlyIleLeuHisAspIleGluGlyIleArgTyrGluProLysCysProLeuGlyValAsp
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                                                                                                                                                                                                                                                                                                                                                                                                                                   CysSerThrMetSerGlyGlyLysAlaIleGluHisLeuAlaLysGlnGlyAsnArgPhe
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CysThrAspAsnGlyIleMetIleAlaTrpAsnGlyIleGluArgLeuArgAlaGlyLeu
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                                                                                              CAAAATAATGCAGTACTGGTTGCATCTGGTTGGTGTCGCAAGTAACTTCTATATCCGCAGA
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOURNAL
MEDLINE
PUBMED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE
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Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altechul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.M.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1211
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web site: http://www.nisc.nih.gov/
Contact: nisc.mgc@nhgri.nih.gov
Akhter, N. Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
Akhter, N. Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
Blakesley, R. W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
Blakesley, R. W., Bouffard, G.G., Breen, K., Gupta, J., Haghighi, P.,
Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Laric, P., Legaspi, R.,
Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,
Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,
McClowell, J., Fearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,
Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
Young, A., Zhang, L.-H. and Green, E.D.
                                                                                                                                                                                                                                                                                                                                                    cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: National Institutes of Health Intramural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (15-SEP-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                                                                               Gaithersburg, Maryland;
                                                                                                                                                                                                                                                                                                                    DNA Sequencing by: National Sequencing Center (NISC),
                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg, R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human and mouse cDNA sequences
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 21312463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ,_
                                       LeuGlnHisValThrAspLySIleIleMetLySLySGluLySGluGlyGluGlyIleGluLyS
                                                                                                                                                                                                       HisPheAspIleLysProProLeuHisHisAlaLysAsnCysAspPheSerPheThrGly
                                                                                                                                                                                                                                                                                                                                                                                             AlaProGlyAspMetLeuAspLysValAlaArgArgLeuSerLeuIleLysHisProGlu
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HisLeuValLysArgThrHisArgAlaIleLeuPheCysLysGlnArgAspLeuLeuPro 140
                                                                                                                                                                                                                                                                                                                                                                        CTGTTGGCATTAGTCCAAGGTGTTTCCGATTTCCTGCTCCTTGGGAAGTCTTTGGACATA
                                                                                                                                                                                                                                                                                    TGTTCTACAATGAGTGGTAGAAAAGCTATAGAACATTTGGCCAAAGACGGAAATAGATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MLMLRRTAGAIPKPPKSKVYGFLRRPSVHPRTLSCHKLVLGIET SCDDTGAAVVDETGNVLGEALHSQTQVHLKTGGIVPVAQQLHRENIQRIVEETLSAS RITPSDLSAIATTIKPGLALSLGVGLSFSLQLVNRFKKPFIPHLMREAHALTIRLTNK VEFFLVLLISGGHCLLALVQGVSDFLLLGKSLDIAPGDMLDKVARRLSLIKHPECST MSGKAIEHLAKDGNRFHFTINPPMQNAKNCDFSFTGLQHITDKLITHKEKEGEIEKG QILSSAADIAAAVQHATACHLAKRTHRAILFCKQKNLLSPANAVLVVSGGVASNLYIR KALEIVANATQCTLLCPPPRLCTDNGIMIAWNGIERLRAGLGVLHDVEDIRYEPKCPLGIDISREVAEAAIKVPRLKWAL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               arose spontaneously from a senescent normal mamma (clonal) outgrowth infected with the virus MWTV."
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/db_xref="CDD:COG0533"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="QRI7; Region: Metal-dependent proteases with
possible chaperone activity [Posttranslational
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="Unknown (protein for MGC:67870)"
/protein_id="AAH58172.1"
/db_xref="GI:34849664"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Mus musculus"
/mol_type="mRNA"
/strain="CZECH II"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="MGC:67870 IMAGE:5012054"
/tissue_type="Mammary tumor metastatized to lung. Tumor
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lab_host="DH10B"
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TITLE
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Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
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Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
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                                                                                                                                                                      Direct Submission
Submitted (25-OCT-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BC038910 1017 bp mRNA linear RO
Mus musculus O-sialoglycoprotein endopeptidase-like 1,
                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.B. Consortium
                                                                                                             NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                   Strausberg, R.
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903
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Best Local Similarity:
Query Match:
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Series:
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info@bcgsc.bc.ca
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AlaLeuGluIleLeuThrAsnAlaThrGlnCysThrLeuLeuCysProProProArgLeu 180
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CTTCAACATATTACTGATAAGCTAATAACACACAGAGGAAAAAGAAGAAGAAGCATTGAGAAA
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                                                     CCAGCTAACGCAGTATTAGTTGTATCTGGAGGTGTTGCAAGTAACTTGTACATCCGAAAA
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/mol_type="mRNA"
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/clone_lib="NCI_CGAP_Li9"
/lab_host="DH10B"
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Patent: EP 1293569-A 400 19-MAR-2003;
Helix Research Institute (JP) ; Resea
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Yamamoto,J.I., Isono,Y., Hio,Y., Otsuka,K., Nagai,K., Irie,R.,
Tamechika,I., Seki,N., Yoshikawa,T., Otsuka,M., Nagahari,K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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                                                          CTTCAACACGTTACTGATAAAATAATGAATAAAGGGAAAAAGGGGAAGGTATTGAGAAG
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400 from Patent EP1293569.
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/mol_type="unassigned DNI
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1436
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Nishi,T., Nakagawa,S., Senoh,A., Mizuguchi,H., Inagaki,H., Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S.,
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J30879 fis, clone FEBRA2004592, highly similar
for putative sialoglycoprotease type 2.
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1 sogai, T., Otsuki, T. and Sugiyama, T.
Direct Submission
Submitted (24-OCT-2001) Takao Isogai, Helix Research Institute,
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
(B-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA library
construction: Helix Research Institute (HRI) (supported by Japan
Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
HRI, and Biotechnology Center, National Institute of Technology and
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                                                                                         HisPheAspIleLysProProLeuHisHisAlaLysAsnCysAspPheSerPheThrGly
                                                                                                                                                                                                                                          GCACCAGGTGACATGCTTGACAAGGTGGCAAGAAGACTTCCTTTAATAAAACATCCAGAG
                                                                                                                                                                                                                                                                                                                               CTGTTGGCATTAGTTCAAGGAGTTTCAGATTTTCTGCTTCTGGAAAGTCTTTGGACATA
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                                                                                                                                                                                       CysSerThrMetSerGlyGlyLysAlaIleGluHisLeuAlaLysGlnGlyAsnArgPhe 60
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/db_xref="GI:16550167"
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/clone_lib="FEBRA2"
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BC078974
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DEFINITION
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                                                                                                                                                                                                                                                                                        RS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gumaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Boutfard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schmerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
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                                                                                   Submitted (02-AUG-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer
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NIH-MGC Project URL: http://mgc.nci.nih.gov
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                                                                                                                                          Direct Submission
                                                                                                                                                                       Director MGC Project.
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                                                         31 Center Drive, Room
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Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA Library Preparation: Express Genomics cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) cDNA Sequencing by: Sequencing Group at the Stanford Human Center, Stanford University School of Medicine, Stanford, edu web site:

http://www-shgc.stanford.edu Contact: (Dickson, Mark) mcd@paxil.stanford.edu Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Howard Ja
                LeuGlnHisValThrAspLysIleIleMetLysLysGluLysGluGluGlyIleGluLys
                                                                                    HisPheAspIleLysProProLeuHisHisAlaLysAsnCysAspPheSerPheThrGly
                                                                                                                                        TGTTCTACAATGAGTGGTGGGAAAGCTATAGAACATTTGGCCAAAGAAGGAAATAGATTC
                                                                                                                                                        CysSerThrMetSerGlyGlyLysAlaIleGluHisLeuAlaLysGlnGlyAsnArgPhe
                                                                                                                                                                                                            AlaProGlyAspMetLeuAspLysValAlaArgArgLeuSerLeuIleLysHisProGlu
                                                                                                                                                                                                                                                                           LeuLeuAlaLeuValGlnGlyValSerAspPheLeuLeuGeuGlyLysSerLeuAspIle
CTTCAACATGTCACCGATAAGCTAATAACACACAAGGAAAAAGAAGAAGAAGCATTGAGAAG
                                                                    CACTITACTATCAATCCACCCATGCAGAATGCTAAGAACTGTGATTTTTCTTTTACGGGA
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QLLSSAADIAAVQHATACHLAKETHALLFCQQKNLLSPANLLVVSGGVASNLYIR
QLLSSAADIAAVQHATACHLAKETHALLFCQXKNLLSPANLVVSGGVASNLYIR
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IVSWLRVLTALTEDLDSVSSTHTVAHSPLNSGSRGANIQTSMCSCTQTVYMRTVRHTL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      db xref="taxon:10116"
/clone="IMAGE:7111906"
/tissue_type="Testis, rat
/clone_lib="NHH_MGC_237"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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|mol_type="mRNA"
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101 GlyGlnIleLeuSerSerAlaAlaAspIleAlaAlaThrValGlnHisThrMetAlaCys
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This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Marcello Bento Soares, Ph.D.
cDNA Library Preparation: M. Bento Soares, University of Iowa
cDNA Library Preparation: M. Bento Soares, University of Iowa
cDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
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Submitted (14-APR-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA Sequencing by: Institute for Systems Biology http://www.systemsbiology.org contact: amadan@systemsbiology.org Anup Madan, Jessica Pahey, Erin Helton, Mark Keti Madan, Stephanie Rodrigues, Amy Sanchez and Mich
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
1 (bases 1 to 1109)
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Mus musculus, clone IMAGE:1327545,
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/db_xref="taxon:10090"
/clone="IMAGE:1327545"
/tissue_type="Thymus gland, mous./clone lib="Soares_thymus_2NbMT"
/lab_host="DH10B"
                                                                                                                                                              /mol_type="mRNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                          organism="Mus musculus"
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Submitted (29-MAR-2004) Sanger Institute, Hinxton, Cambridgeshire,
Submitted (XI) Mix. B-mail enquiries: chickest@bms.umist.ac.uk
On Apr 1, 2004 this sequence version replaced gi:41631222.
BBSRC/Dundee/Nottingham/Sanger/Sheffield/UMIST Gallus gallus cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 LeuLeuAlaLeuValGlnGlyValSerAspPheLeuLeuLeuGlyLysSerLeuAspIle :::||||||:::||||||||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BBSRC/Dundee/Nottingham/Sanger/Sheffield/UMIST cDNA collection, from a library constructed by Elizabeth Bosch. cDNA was prepared from RNA extracted from limbs, normalised, and poly A-trimmed. EcoRI-NotI cut cDNA was then ligated into the vector: Vector: pBluescript II KS(+); Site_1: EcoRI; Site_2: NotI Host: Escherichia coli DH10B.
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Boardman, P.B., Bonfield, J.K., Brown, W.R.A., Carder, C., Chalk, S.B., Croning, M.D.R., Davies, R.M., Francis, M.D., Grafham, D.V., Hubbard, S.J., Humphray, S.J., Hunt, P.J., Maddison, M., McLaren, S.R., Niblett, D., Overton, I.M., Rogers, J., Scott, C.B., Taylor, R.G., Tickle, C. and Wilson, S.A.
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                                                          HisLeuValLysArgThrHisArgAlaIleLeuPheCysLysGlnArgAspLeuLeuPro 140
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GlnAsnAsnAlaValLeuValAlaSerGlyGlyValAlaSerAsnPheTyrIleArgArg 160
                                                                                                                                                                        GlyGlnIleLeuSerSerAlaAlaAspIleAlaAlaThrValGlnHisThrMetAlaCys 120
                                                                                                                                                                                                                                                                                                                        GCACCAGGTGACATGCTGGATAAGGTAGCAAGAAGGCTCTCTTTAGTGAAGCACCCGGAG
                                                                                                                                             GGGGAAATCCTGTCCTGCGTTAAGGACATCGCTGCTGCTGCACAGCACGTAGTGGCTGCT
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/strain="White Leghorn,
/db_xref="taxon:9031"
/clone="ChEST967o14"
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Search completed: June 16, 2005, 23:18:47 Job time : 2866.39 secs	754 ATTTCCAAAAGAGTTGAAGAGGATTCCATCAAAGTGCCAAGACTAAGG 801	221 IleSerLysGluValGlyGluAlaSerIleLysValProGlnLeuLys 236	694 GGTATTTTATACAGTACTGATGGCATCCGCTACGAACCAAAAGCTCCCCTTGGAATTGAT 753	201 GlyIleLeuHisAspIleGluGlyIleArgTyrGluProLysCysProLeuGlyValAsp 220	634 TGCACCGATAATGGTGTTATGATTGCATGGAATGGCATTGAAAGGTTGCGTGCAGGATGT 693	181 CysThrAspAsnGlyIleMetIleAlaTrpAsnGlyIleGluArgLeuArgAlaGlyLeu 200	574 GGACTGCAGACTCTGGCAAATGCAAACGGTTTTGCTTTTCTGTCTCCTCCTCCAAGGCTG 633	161 AlaLeuGluIleLeuThrAsnAlaThrGlnCysThrLeuLeuCysProProProArgLeu 180

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-Q=/cgn2 1/USPTO_spool_p/US10649273/runat_15062005_111415_6022/app_query.fasta_1.1429
-DB=N_Geneseq_16Dec04 -QFMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODES-LOCAL -OUTFMT=pto -NORM=ext -HRAPSIZES=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10649273_0GGN 1 1063_9runat_15062005_111415_6022 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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1: geneseqn1980s:*
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4: geneseqn2001as:*
5: geneseqn2002as:*
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Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cancer and tumours; and inflammatory diseases (e.g. septic shock, Crohn's disease, anaphylaxis). The protein may be used to inhibit the growth, infection or function of infectious agents such as bacteria, fungi, viruses, or to effect bodily characteristics, biorhythms or circadian cycles of rhythms. The protein may also have proliferation/differentiation, stem cell growth factor, haematopoiesis regulation, immune stimulating or suppressing, chemotactic/chemokinetic, haemostatic and thrombolytic, receptor/ligand, and antiinflammatory activities. The cDNA sequences of the invention are useful for expressing recombinant protein for analysis. The present sequence represents a novel human cDNA sequence of the invention, this sequence is an expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel polypeptide useful for treating neurodegenerative diseases, my or lymphoid cell disorders, bone disorders, mechanical and traumatic disorders, coagulation disorders, and inflammatory diseases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Metalloprotease; MP-1; immune disorder; glutamate transport; cancer; motor neuron disorder; amyotrophic lateral sclerosis; ALS; diabetes; reproductive disorder; Kleinfelter's syndrome; germinal cell aplasia; genital wart; metabolic disorder; premature puberty; Kallman syndrome; Cushing's syndrome; neurodegenerative disease; Alzheimer's disease; Parkinson's disease; Huntington's disease; Tourette syndrome; sepsis; liver disease; renal disease; immune disorder; rheumatoid arthritis; acquired immunodeficiency syndrome; AIDS; pulmonary disease; pneumonia emphysema; cystic fibrosis; vascular disorder; inflammatory disorder;
                           New isolated nucleic acid encoding MP-1 protein, useful for preventing, treating, or ameliorating diseases associated with aberrant metalloproteinase activity, e.g. immune, metabolic, inflammatory and
                                                                                                                                                                                                                                                                                                                                                           05-FEB-2001;
10-APR-2001;
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                     metalloproteinase activity, e.g. immune,
                                                                                                                                                                               WPI; 2002-723329/78.
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Disclosure; Page 462-463; 473pp; English.

metalloprotease (MP-1). (I) is useful for preventing, treating, or ameliorating a medical condition, particularly an immune disorder, an electrophic lateral sclerosis (ALS) its juvenile form or an ALS-like condition. The compositions and methods are also useful for diagnosing, prognosticating, treating, ameliorating and/or treating disorders (e.g. Kleinfelter's syndrome, genital warts, or germinal cell associated with MP-1 activity, e.g. diabetes, cancer, reproductive CC aplasia), metabolic disorders (e.g. premature puberty, Kallman syndrome, or CC or Cushing's syndrome), neurodegenerative diseases (Alzheimer's disease, Huntington's disease or Tourette syndrome), liver and renal diseases and immune disorders (e.g. AlDS, rheumatoid arrhritis CC or sepsis), pulmonary diseases (e.g. pneumonia, emphysema or cystic CC fibrosis) and vascular, inflammatory and neurological disorders (e.g. Alzheimer's disease or Parkinson's disease). This sequence represents a CC metalloprotease MP1 polynucleotide describes an isolated nucleic acid molecule (I) encoding

Sequence 1526 BP; 484 A; 297 C; 289 <u>ი</u> 456 ;; 0 **∵** 0 Other;

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LeuGlnHisValThrAspLysIleIleMetLysLysGluLysGluGluGlyIleGluLys 100
                                                                                                                                                                                                                                                                                            HisPheAspIleLysProProLeuHisHisAlaLysAsnCysAspPheSerPheThrGly
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                                                         AlaLeuGluIleLeuThrAsnAlaThrGlnCysThrLeuLeuCysProProProArgLeu
                                                                                                         GlnAsnAsnAlaValLeuValAlaSerGlyGlyValAlaSerAsnPheTyrIleArgArg
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                                              GCTCTGGAAATTTTAACAAACGCAACACAGTGCACTTTGTTGTGTCCTCCTCCCAGACTA
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                                                                                                                                                                                                          Pred. No.:
                                                                                                                                                                                                                                    Alignment
                                                                                                                                                                                                                                                                                                                                       The present sequence encodes human O-sialoglycoproteinase-like protein (OSGPLP). The present invention also describes: (1) the preparation of the OSGPLP protein; (2) applying the OSGPLP protein in diagnosis; (3) the prevention and/or treatment of related diseases; (4) utilising the OSGPLP protein in screening its agonist, excitomotor and inhibitor and preparing an antibody against the OSGPLP protein; and (5) the use of the OSGPLP polymucleotide sequences, proteins, agonists, excitomotors, inhibitors and antibodies in treating diseases related to the abnormal OSGPLP gene and in preparing the medicine composite for the treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mao
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                                                                                                                                                                                                                                                                                           Sequence 2058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 5; Page 29-30 (Disclosure); 38pp; Chinese.
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05-FEB-2002; 2002WO-US003353

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121 HisLeuValLysArgThrHisArgAlaIleLeuPheCysLysGlnArgAspLeuLeuPro

140 1115 1055 100 80

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19-SEP-2002.

WO200272751-A2

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2197 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention describes an isolated nucleic acid molecule (I) encounteralloprotease (MP-1). (I) is useful for preventing, treating, or ameliorating a medical condition, particularly an immune disorder,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated nucleic acid encoding MP-1 protein, useful for preventing, treating, or ameliorating diseases associated with aberrant metalloproteinase activity, e.g. immune, metabolic, inflammatory and
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10-APR-2001;
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                                                                                              LeuGlnHisValThrAspLysIleIleMetLysLysGluLysGluGlyIleGluLys
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                  GlyGlnIleLeuSerSerAlaAlaAspIleAlaAlaThrValGlnHisThrMetAlaCys 120
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                                                                           CTTCAACACGTTACTGATAAAATAATAATGAAAAAGGAAAAAGAGGAAGGTATTGAGAAG
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06-JUL-2001; 2001US-0303445P.
13-JUL-2001; 2001US-0305405P.
09-AUG-2001; 2001US-0311442P.
24-AUG-2001; 2001US-0314921P.
29-AUG-2001; 2001US-0315992P.
03-MAY-2002; 2002US-0378205P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antiulcer; hepatotropic; gynaecological; antibacterial; virucide; protozoacide; antiparasitic; cell proliferative disease; PMOD; protein modification and maintenance molecule; immunogenic fragment; cancer; autoimmune; inflammatory disease; neurological disorder; gastrointestinal; developmental; vesicle trafficking disorder; infection; protein-protein interaction; drug-target interaction; gene expression profile; human; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cytostatic; antiarteriosclerotic; anti-HIV; antiallergic; anticonvulsant; cerebroprotective; antiparkinsonian; nootropic; antiinflammatory; antiulcer; hepatotropic; gynaecological; antibacterial; virucide;
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New isolated human PMOD polypeptide and polynucleotide, useful for diagnosing, treating and preventing diseases or conditions associated with the aberrant PMOD expression, e.g. cancer, AIDS, atherosclerosis
                                                                                                                                                                                                                                                              Thangavelu K, Gietz
Walia NK, Mason PM,
Elliott VS, Luo W,
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Thangavelu K, Gietzen KJ,
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                                                                                                                                                                                                                                                          Warnakar A, Hafalia AJA, Tran B, Duggan BM Honchell CD, Nguyen DB, Lu DAM, Lee BA, Yue o I, Ramkumar J, Griffin JA, Li JX, Yang J; en KJ, Ding L, Baughn MR, Borowsky ML, Yao MG Gururajan R, Lee S, Becha SD, Lee SY, Tran Sprague WM, Tang YT, Lu Y, Zebarjadian Y;
                                                                                                                                                                                                                                                                                                                                        Yang J;
L, Yao MG;
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Best Local Similarity: Query Match: Percent Similarity:

1240.00 100.00% 100.00% 7.47e-132

Mismatches: Indels: Matches: Conservative:

2572 239 0 0 0

Score:

Alignment Scores: Pred. No.:

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The invention relates to an isolated polypeptide comprising: any of 28 cc sequences of 48-1256 amino acids; a natural amino acid sequence at least CC 90% identical to the 28 amino acid sequences, 94% identical to a sequence co of 703 or 267 amino acids, 96% identical to a sequence of 414 amino coids, or 97% identical to a sequence of 642 amino acids, all given in CC the specification; or a biologically active or immunogenic fragment of CC with the decreased expression of protein modification and maintenance complexity in the decreased expression of protein modification and maintenance complexity. The polypeptides and polymucleotides are useful complexity in the decreased expression of protein modification and maintenance complexity. The polypeptides are useful complexity in a second expression of protein modification and maintenance complexity. The polypeptides is grown, parkingon's disease, complexity. The polypeptides is grown, parkingon's disease, complexity. The polypeptides is grown and discretive (e.g. allergies), aparticipation in a session the expression of the complexity of proteonally. These are also compounds on the expression of mucleic acid and amino acid sequences of pMOD. The pMOD or its compounds on the expression of the compounds to the polypeptides, or in altering the expression of the target polymucleotide and compounds that specifically bind to or modulate compounds in the polypeptide. The microarray is useful in monitoring compounds on the expression of the activity of the polypeptide. The microarray is useful in monitoring compounds on the polypeptide. The microarray is useful in monitoring compounds on the polypeptide. The microarray is useful in monitoring compounds on the polypeptide. The microarray is useful in monitoring compounds on the polypeptide. The microarray is useful in monitoring compounds in the polypeptide. The microarray is useful in monitoring compounds in the polypeptide. The microarray is useful in monitoring compounds in the polypeptides of the polypeptides of the poly
Claim 91; Page 211; 225pp; English
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Sequence 2572 BP; 780 A; 489 C; 509 G; 794 T; 0 U; 0 Other;

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                                                                                                                                           LeuGlnHisValThrAspLysIleIleMetLysLysGluLysGluGlvGlvIleGluLys
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                                                                                     GGGCAAATCCTGTCTTCAGCAGCAGACATTGCTGCCACAGTACAGCACACAATGGCATGT
                                                                                                GlyGlnIleLeuSerSerAlaAlaAspIleAlaAlaThrValGlnHisThrMetAlaCys
                                                                                                                              CTTCAACACGTTACTGATAAAATAATAATGAAAAAGGGAAAAAGAGGGAAGGTATTGAGAAA
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                                           CATCTTGTGAAAAAGAACACATCGGGCTATTCTGTTTTGTAAGCAGAGAGACTTGTTACCT
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                                                                                                                                                                                                                                                            08-NOV-2000; 2000US-0246768P.
08-NOV-2000; 2000US-0246772P
15-NOV-2000; 2000US-0249185P
The present invention relates to novel 38650, 28472, 5495, 65507, 81588 or 14354 nucleic acid molecules which encode adenosine deaminase, glycoprotease or seven transmembrane domain (7TM) receptor family members. Sequences of the invention are useful in diagnosing and treating cancer
                                                                                                       New 38650, 28472, 5495, 65507, 81588 or 14354 nucleic acid molecules, useful for diagnosing and treating cancer, immune, cardiovascular, hematopoietic, brain, pain, metabolic, liver or platelet disorders, a
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/note= "This region is specifically claimed
6 in claim 1 of the specification"
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or aberrant cellular proliferation and/or differentiation (e.g. colon or clump cancer), immune disorders (e.g. selective IGA deficiency, rheumatoid arthritis, diabetes, allergy), heart or cardiovascular disorders (e.g., hypertension, atherosclerosis, arrhythmias, ischaemic heart disease, myocardial infarction, thrombus) including endothelial cell disorders (e.g. psoriasis, Grave's disease), haematopoietic disorders, brain cliding endothelial cell disorders (e.g. psoriasis, Grave's disease), haematopoietic disorders, brain cliding endothelial cell disorders (e.g. psoriasis, Grave's disease), liver disorders or platelet disorders (e.g. obseity), liver disorders or platelet chisorders. They are also useful in screening assays, predictive medicine (e.g. diagnostic assays, prognostic assays, monitoring clinical trials and pharmacogenetics) and prophylactic and therapeutic methods. The nucleic acids may also be used in chromosome mapping, tissue typing and forensic biology and as surrogate markers. Sequences of the invention are also used in gene therapy. The present sequence is human glycoprotease
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28472 cDNA
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Sequence 1820 B₽; 543 A, 365 Ç 393 ູດ 518 7 0 U; 1 Other;

Query Match: DB:

Best Local Similarity: Percent Similarity:

8.22e-128 1203.00 98.33% 97.07% 97.02%

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                               GGCATTTTACATGACATAGAAGGCATCCGCTATGAACCAAAATGTCCTCTTGGAGTAGAC
                                                GlyIleLeuHisAspIleGluGlyIleArgTyrGluProLysCysProLeuGlyValAsp
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deaminase), 28472 (enroding a glycoprotease), 5495 (enroding a 7 cd deaminase), 28472 (enroding a glycoprotease), 5495 (enroding a 7 cd transmembrane receptor), 65507, 81588 or 14354 nucleic acid molecule (or 2 sequence which is at least 60% identical to the six nucleic acids or 2 their open reading frames, fragments of at least 15 nucleotides, 2 naturally occurring variants, or a DNA insert of the plasmid deposited 2 with the American Type Culture Collection as Accession No. not defined in 2 cd are a host cell containing the nucleic acids (used to produce the 2 proteins), the encoded proteins, an antibody that selectively binds to 2 cd proteins), the encoded proteins, an antibody that belocute the 2 cd polypeptide, and identifying a compound that binds to/modulates the 2 cd polypeptide, and identifying a compound that binds to/modulates the 2 consideration and/or differentiation, immune disorders, heart disorders, 2 consideration and/or differentiation, immune disorders, heart disorders, 2 cd namatopoeitic disorders including endothelial cell disorders, pain 3 cd and miclabolic disorders, liver disorders and platelet disorders (many 2 camples of these disorders are given in the specification). The present
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P-PSDB;
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08-NOV-2000; 2000US-0246772P.
15-NOV-2000; 2000US-0249185P.
                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated 38650, 28472, 5495, 65507, 81588 and 14354 nucleic acid molecules, useful for diagnosing, treating cancer, pain, or immune, heart, endothelial cell, hematopoeitic, blood vessel, brain, metabolic
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(KAPE/) KAPELLER-LIBERMANN
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/product= "Glycoprotease"
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08-NOV-2000; 2000US-0246772P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2208
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/or membrane proteins, useful for developing medicines for diseases
ch the gene is involved, or as target molecules for gene therapy.
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                                           AlaLeuGluIleLeuThrAsnAlaThrGlnCysThrLeuLeuCysProProProArqLeu 180
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Otsuka M, Nagahari K, Mas¤
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Query Match: DB:

Percent Similarity: Best Local Similarity:

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                                                         The invention relates to a novel method for detecting soft tissue sarcoma which comprises obtaining a first soft tissue sample from an individual and a normal soft tissue sample from the same or different individual, determining the expression of a gene in both samples and comparing the expression of the gene in both soft tissue samples and comparing the presence of soft tissue sarcoma. The method of the invention has cytostatic applications and may be useful for detecting soft tissue sarcoma, possibly via gene therapy or vaccine production. The nucleic acid sequences may be useful in diagnostic and screening applications. The current sequence is that of a human soft tissue sarcoma-upregulated DNA of the invention. The current sequence is that of a human soft tissue sarcoma within the specification per se but was submitted in CD format by the inventor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Early detection of soft tissue sarcoma comprises determining expression of a gene in a first soft tissue sample and a normal soft tissue sample and comparing the gene expression, also useful in treating soft tissue
   Sequence 2890 BP;
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          12 Other;
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RESULT 11
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                                       antiinflammatory; cerebroprotective; antilipaemic; antidiabetic; immunosuppressive; neuroprotective; nootroplic; neuroleptic; tranquilizer; osteopathic; antiarthritic; antirheumatic; cytostaatic; hepatotropic; virucide; haemostatic; anti-HIV; antithyroid; thyromimetic;
dermatological; antibacterial; fungicide; antiparasitic; anticonvulsant;
thrombolytic; anticoagulant; anorectic; vasotropic; antiulcer;
                                                                                                                                   diagnostic and therapeutic polynucleotide; dithp; antiarteriosclerotic;
                                                                                                                                                                                Human diagnostic and therapeutic polynucleotide (dithp), SEQ ID No 100.
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CC comprising a naturally occurring polynucleotide sequence at least 90% contentical to the dithp polynucleotide; a polynucleotide complementary to the dithp polynucleotide or its polynucleotide which is at least 90% contentical; or an RNA equivalent of any of the polynucleotides mentioned above. The dithp polynucleotides have the following activities: cantitarteriosclerotic, antiinflammatory, cerebroprotective, antilipaemic, contropic, neuroleptic, controlication, neuroleptic, controlication, neuroleptic, controlication, neuroleptic, controlication, neuroleptic, controlication, neuroleptic, controlication, neuroleptic, controlication, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic, neuroleptic
                                                                               Hashimoto's thyroiditis, multiple sclerosis, osteoarthritis, rheumatoid arthritis, scleroderma, systemic lupus erythematosus), infections (e.g. viral, bactérial, fungal or parasitic infection), developmental disorders (e.g. Cushing's syndrome or epilepsy), endocrine disorders (e.g. thrombosis, hypopituitarism, hypogonadism, gigantism, goiter) metabolic disorders (e.g. hypercholesterolaemia, hypoglycaemia, diabetes, hyperlipidaemia, obesity), neurological disorders (e.g. ischaemic cerebrovascular disease, stroke, Alzheimer's disease, Pick's disease, Huntington's disease, Parkinson's disease, Creutzfeldt-Jakob disease, anxiety, schizophrenia), gastrointestinal disorders (e.g. ulcers), transport disorders (e.g. akinesia or multidrug resistance), or connective tissue disorders (e.g. Paget's disease or rickets). This polymucleotide sequence represents one of the human dithp DNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New human diagnostic and therapeutic polynucleotides and polypeptides, useful for diagnosing, treating or preventing e.g. leukemia, brain cancer, atherosclerosis, AIDS, thyroiditis, infections, obesity, stroke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a novel isolated human diagnostic and therapeutic polynucleotide (designated dithp). The novel dithp polynucleotide comprises: any of 188 DNA sequences consisting of base pairs fully defined in the specification; a polynucleotide
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Kristnam SR,
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17-JAN-2002; 2002US-0349413P.
17-JAN-2002; 2002US-0349946P.
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Tuason O, Yap PE, Amshey SR, Dan
ta CH, Lewis SA, Chen A, Marwaha R,
nam SR, Kolluru V, Panesar IS;
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Sequence 3358 BP; 1105 A; 577 Ç 601 G; 1075 Ŧ; 0 U; 0 Other

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Percent Similarity: Best Local Similarity: Score: Pred. No.: 1.4e-103 995.50 87.82% 87.82% 80.28% Length: Matches: Mismatches: Indels: 3358 209 0 2 2 29

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                               05-DEC-2001; 2001WO-US046405
                                                                                                                                                                                                                                                                                                                                            Murine; mouse; protease; calcium activated neutral protease type 5;
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CC comprising a disruption in a protease target gene (PG) selected from CC calcium activated neutral protease type 5 (CAPN5) gene, tryptase 4 gene CC and sialoglycoprotease-like gene. Also described is a targeting construct comprising a first polymucleotide sequence homologous to at least a confirst portion of PG, a second polymucleotide sequence homologous to at comprising a first polymucleotide sequence homologous to at least a second portion of PG and a selectable marker. (II) is useful for CC producing a transgenic mouse comprising a disruption in a protease target CC gene, by introducing (II) into a cell, introducing the cell into a CD blastocyst, implanting the resulting blastocyst into a pseudopregnant CC mouse, where the pseudopregnant mouse gives birth to a chimeric mouse, and breeding the chimeric mouse to produce the transgenic mouse. (I) is confirmed to resulting blastocyst into a pseudopregnant consecution of a protease target gene, by administering an agent to (I) and CC determining whether the expression or function of the disrupted protease target gene by administering an agent to (I) and CC efficacy of proposed genetic and pharmacological therapies for human CC genetic diseases, such as neurological, neuropsychological or psychotic illness. The present sequence represents murine sialoglycoprotease-like gene sequence, which is used in an example from the present invention
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06-DEC-2000;
13-DEC-2000;
Sequence 1572
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 3; Fig 7; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           with a disruption in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel transgenic animal, comprising a disruption in protease target gene, is useful for identifying agents that ameliorates a phenotype associated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               present invention describes a non-human transgenic animal (I)
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2000US-0251820P.
2000US-0255971P.
BP; 459 A; 337
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  C; 340
  G; 429 T; 0 U; 7 Other;
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GlyGlnIleLeuSerSerAlaAlaAspIleAlaAlaThrValGlnHisThrMetAlaCys
                                    CysSerThrMetSerGlyGlyLysAlaIleGluHisLeuAlaLysGlnGlyAsnArgPhe
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                                                                                                                                                                                                     LeuLeuAlaLeuValGlnGlyValSerAspPheLeuLeuLeuGlyLysSerLeuAspIle
                                                                         HisPheAspIleLysProProLeuHisHisAlaLysAsnCysAspPheSerPheThrGly
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sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders
                                                                                                                                               The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain
                                                                                                                                                                                                                                              New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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23-AUG-2000; 2000US-00649167.
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                                                                                                              standard;
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                                                                                                                                                                                                  AspIleGluGlyIleArgTyrGluProLys-----CysProLeuGlyVal 219
                                                                                                                                                                                                                                              GGCATTATGAAATGCATGAATGGTATTGAAAGACTACGTGCTGGCTTTGGGCATTTTACAT
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20-MAY-2004

(first entry)

DNA up-regulated in murine multipotent progenitor cells

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 8; SEQ ID NO 3118; 123pp; English.
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multipotent progenitor; MPP; common lymphoid progenitor; CLP;
on myeloid progenitor; CMP; bone marrow stem cell; mouse; murine; ds.
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                                                                                                                                                                                                                                                                                                                                 AlaIleLeuPheCysLysGlnArgAspLeuLeuProGlnAsnAsnAlaValLeuValAla 148
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US-10-649-273-2_COPY_176_414 (1-239) x ADL86726 (1-371)
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-Q-/Ggn2 1/USPTO, Spool p/US10649273/runat_15062005_111417_6057/app_query.fasta_1.1429
-DB-Issued Patents NA -QPMT=fastap -SUFFIX=p2n.rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS-bits -START=1 -END=-1 --MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORR=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10649273 @CGN 1 1 177 @runat 15062005 111417 6057 -NCPU=6 -ICPU=3
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
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Sequence 21, Appl
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Sequence 806, App
Sequence 801, App
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Sequence 794, App Sequence 131, App Sequence 3566, Ap	10	1618, e 1, A e 1, A p	Sequence 6, Appli Sequence 261, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli	21,	Sequence 1, Appli Sequence 51, Appl Sequence 51, Appl Sequence 1072, Ap	147,	2955, 5, Ap 3, Ap 727,	

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                                                                                                  NUMBER OF SEQ ID NOS: 441
SOFTWARE: pt_FL_genes Version 2.0
SEQ ID NO 177
                                                                                                                                                                                    APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6743619el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
                                                                                                                                             FILE REFERENCE: 802
CURRENT APPLICATION NUMBER: US/09/774,528
CURRENT FILING DATE: 2001-01-30
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                                                        TYPE: DNA
ORGANISM: Homo
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Zhao, Qing A.
Yang, Yonghong
Xue, Aidong J.
Wehrman, Tom
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Wang, Dunrui
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Asundi, Vinod
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Alignment Scores:

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Query Match:
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Best Local Similarity:
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    GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLECTIDE ENCODING A NOVEL METALOPROTEASE HIGHLY EXPRESSED
TITLE OF INVENTION: SPINAL CORD, MP-1
FILE REFERENCE: D0073 NP
CURRENT APPLICATION NUMBER: US/10/067,443
CURRENT FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
PRIOR FILING DATE: 2001-02-05
PRIOR FILING DATE: 2001-04-10
PRIOR FILING DATE: 2001-04-10
                                                                                                                                                                  Sequence 23, Application US/10067443 Patent No. 6642041
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                                                                                                                                                                                                                                                                                                             GlyIleLeuHisAspIleGluGlyIleArgTyrGluProLysCysProLeuGlyValAsp 220
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GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLBOTIDE ENCODING
TITLE OF INVENTION: SPINAL CORD, MP-1
                                                    Sequence 1, Application Patent No. 6642041
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; LENGTH: 1526
; TYPE: DNA
; ORGANISM: homo :
US-10-067-443-23
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ATATCAAAAGAAGTTGGAGAAGCTTCCATAAAAGTACCACAATTAAAAATGGAGATA
               IleSerLysGluValGlyGluAlaSerIleLysValProGlnLeuLysMetGluIle
                                                         GGCATTTTACATGACATAGAAGGCATCCGCTATGAACCAAAATGTCCTCTTGGAGTAGAC
                                                                         GlyIleLeuHisAspIleGluGlyIleArgTyrGluProLysCysProLeuGlyValAsp|
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NOVEL METALOPROTEASE HIGHLY

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FILE REFERENCE: D0073 NP
CURRENT APPLICATION NUMBER: US/10/067,443
CURRENT FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR PILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR PILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 1
LENGTH: 2197
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LOCATION: (231)..(1472)
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ORGANISM: Homo
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                                                  GlyIleLeuHisAspIleGluGlyIleArgTyrGluProLysCysProLeuGlyValAsp 220
                                                                                                                       CysThrAspAsnGlyIleMetIleAlaTrpAsnGlyIleGluArgLeuArgAlaGlyLeu 200
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IleSerLysGluValGlyGluAlaSerIleLysValProGlnLeuLysMetGluIle 239
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; ORGANISM: homo
US-10-067-443-21
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APPLICANT: Bristol-Myers Squibb Company
APPLICANT: Bristol-Myers Squibb ENCODING A NOVEL METALOPROTEASE HIGHLY EXPRESSED
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE HIGHLY EXPRESSED
TITLE OF INVENTION: SPINAL CORD, MP-1
FILE REPERENCE: DO073 NP
CURRENT APPLICATION NUMBER: US/10/067,443
CURRENT FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR TILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
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PheTyrIleArgArgAlaLeuGluIleLeuThrAsnAlaThrGlnCysThrLeuLeuCys 175
                            HisThrMetAlaCysHisLeuValLysArgThrHisArgAlaIleLeuPheCysLysGln 135
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123	GlyIleGluLysGlyGlnIl 103 	IleMetLysGluLysGluGlu96 	CTTTTACTGGACTTCAACACGTTACTGATAAAATA	88	GCCATAGAACATTIGGCCAAACAAGGAAATAGATTICATTITGACATCAAACCTCCCTIG 11959	•	ValAlaArgArgLeuSerLeuIleLysHisProGluCysSerThrMetSerGlyGlyLys 48 	_COPY_1/6_414 (1-239) x US-10-06/-443-20 (1-14364)	:	32.86% 58.47%	Matches: Conservative:	o,		sapiens		PatentIn version 3.0	PRIOR FILING DATE: 2001-04-10 NUMBER OF SEO ID NOS: 71	FILING DATE: 2001-02-05 APPLICATION NUMBER: US 60/282 814	CURRENT FILING DATE: 200/205 PRIOR APPILICATION NIMBER: 13 60/266 518	FILE REFERENCE: D0073 NTWDEED IN /10/07 //2	AFFLICANI: BIISCOI-MYETS SQUIDD COMPANY TITLE OF INVENTION: POLYNIC COED MD 1 TITLE OF INVENTION: COLUMN COED MD 1	GENERAL INFORMATION:	Requence 20, Application US/10067443		AAAATGGAGATA 1340	remetGluIle 239	GAGTAGACATATCAAAAGAAGTTGGAGAAGCTTCCATAAAAGTACCACAATTA 1328	roLeuGlyValAspIleSerLysGluValGlyGluAlaSerIleLysValProGlnLeu 235 	THE THE THE THE TENTH OF THE TE	.laGlyLeuGlyIleLeuHisAspIleGluGlyIleArgTyrGluProLysCys 215	roProProArgLeuCysThrAspAsnGlyIleMetIleAlaTrpAsnGlyIleGluArg 195 	
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151 yValAlaSerAsnPheTyrIleArgAlgAlaLeuGluIleLeuThrAsnAlaThrGlnCy	13160 TCATATCCATATATGATAGTTATTTTGGTTTTCTCAATTCCTTCAGGTTGCATCTGGTGG	GGGATAGTTTATTGTTTAATGCTGATATTTTTCTCCAGGTTTA	13040 TTTTTCTTTCCAAATTTTTATTACATAGATATGTCATCTGCCCATTACCCATCTCAAAAT 13099		12980 TGGAAGAAAATATACAAAAATGCTAGTAATGTTTGTATGCTATTAGAATTATTAGTAATT	146	12920 AGGGTCTAAAATAGTGTACTATGATTGAAATTATATATAAATAA	146	12860 ATATCAAAGAATAATTTTTTCAGAGTTATGTAGTAAAATGCACAAAATAATAAAAAATTTC	146	12800 TATAAACTAAAGTGGGAAAATGTTTAAATGGTAGTAATTCATAGATGGAATTTTACATGG	146	12740 CTTAAAAGCCTTGACAAACATCCTGTTTAACTGTATCTTAAACTTTATTCATTTAAAAAT 12799	146	12680 AATGTTGATAAAGTTCTGATAATCCACTATATTGTACCAGCCAAAATCCCCTTTAATTGTG	146	12620 TTTTTTAATAAGCCAGTCAAATTTAGCAGTGGGAGGTGGTATTCCAACTTTCGTGACACT 12679	146	12560 ATTTTTAGAAAAATAGGTGGATTTCCTTCATCCTTTGATGAAATCCCTTTGTTTG	146	12500 CTTGTTGGATTTAAAAGAGGGCTTACAATAAAGAAAGTAAATGCAGTAACTGCTATCACT	146	12440 TGGTAGCTTTATGGGACAGCTGTATAGCTTCTATGGCACATAAGTCTAATTTTGCATCTT	146	12380 CCCTGACAGTATGAAATTATGCAGGATAGGAAAGACTAACAGCCATTTCTTGTACTAGTT	146	12320 TTTTTTCCCAAGACCTTGACCTTGTGTTTAGGATGAACAGATCTTTATGCCTTATGCTAG	146		143 nAlaValLeu	123 llysArgThrHisArgAlaIleLeuPheCysLysGlnArgAspLeuLeuProGlnAsnAs 	

Qy 61 HisPheAspIleLysProProLeuHisHisAlaLysAsnCysAspPheSerPheThrGly ::::::::	Qy 41 CysSerThrMetSerGlyGlyLysAlaIleGluHisLeuAlaLysGlnGlyAsnArgPhe	Qy 21 AlaProGlyAspMetLeuAspLysValAlaArgArgLeuSerLeuIleLysHisProGlu	Qy 1 LeuLeuAlaLeuValGlnGlyValSerAspPheLeuLeuGlyLysSerLeuAspIle ::: :::	US-10-649-273-2_COPY_176_414 (1-239) x US-09-596-002-38 (1-94750)	Alignment Scores: Pred. No.: \$248.50	P - 21	PERL Prog 38 94750 A	CURRENT FILLING DATE: 2000-06-16; PRIOR APPLICATION NUMBER: 60/140,121; PRIOR FILING DATE: 1999-06-18; NUMBER OF SEQ ID NOS: 41	Chandra L. CLEOTIDE SEQUENCES OF MORAXELLA CATARRHALIS B-4 US CEP 100 100 100 100 100 100 100 100 100 10	RESULT 6 US-09-596-002-38 US-09-596-002-38 ; Sequence 38, Application US/09596002 ; Patent No. 6632636 ; GENERAL INFORMATION: ; APPLICANT: Lagace, Robert, E.	Db 13520 GCTATGAACCAAAG 13533	Qy 210 rgTyrGluProLys 214	Db 13460 GGAATGGTATTGAAAGACTACGTGCTGGCTTGGGCATTTTACATGACATAGAAGGCA	Qy 191AsmGlyIleGluArgLeuArgAlaGlyLeuGlyIleLeuHisAspIleGluGlyIleA	Db 13400 ACTAAGCCTTCTTCCTTCAGATCTTGGAGCTATTGATTTTATTTTAATGCTTCTTATTTA	Оу 190	Db . 13340 AGCCACAGGATATACGTGCTTCACTCATAACTATGTAAATATTAATTGCCATTTTATCAT	Оу 190	Db 13280 CACTTTGTTGTGTCCTCCCCAGACTATGCACTGATAATGGCATTATGCATTGCATGGTA	
PheSerPheThrGly 80 ::: TTTTCGTTCAGTGGC 24520	GInGlyAsnArgPhe 60 aacccaaccacac 24463	IleLysHisProGlu 40 CCCTATCCT 24418	LysSerLeuAsplle 20 ::: ::: CAGTCTATCGATGAT 24364	9475					ATARRHALIS GENOME				ACATAGAAGGCATCC 13519	spileGluGlyIleA 210	AATGCTTCTTATTTA 13459	190	TIGCCATITIATCAT 13399	190	TATGATTGCATGGTA 13339	

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Best Local Similarity:
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US-09-540-236-806
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Sequence 806, Application US/09540236
Patent No. 6673910
PATENT INFORMATION:
APPLICANT: Gary L. Breton et al.
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 3840 SEQ ID NO 806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: 2709.2005-001
CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT FILING DATE: 2000-04-04
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TYPE: DNA
ORGANISM: M.catarrhalis
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                        CysSerThrMetSerGlyGlyLysAlaIleGluHisLeuAlaLysGlnGlyAsnArgPhe
                                                                                                          AlaProGlyAspMetLeuAspLysValAlaArgArgLeuSerLeuIleLysHisProGlu 40
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                                                                              GCGGTGGGCGAATGCTTTGATAAAACGGCAAAAATGCTCAAACTG---CCCTATCCT---
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247.00
46.85%
31.53%
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    -GGTGGTCCAAATATCGAAAAATTAGCCAAAAACGGCAACCCCACAC 603
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Matches:
Conservative:
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                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: NUCLEIC ACID AND AMINO ATTILE OF INVENTION: AERUGINOSA FOR DIAGNOSTIFILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
PRIOR FILING DATE: 1998-07-27
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                                                                                                                                     Query Match:
                                                                                                                                                                    Percent Similarity:
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                                                                                                                                                                                                                                                                       SEQ ID NO 884
LENGTH: 1059
TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                         ORGANISM: Pseudomonas
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ProGlyAspMetLeuAspLysValAlaArgArgLeuSerLeuIleLysHisProGluCys 41
                              TTGGTGCGGGTGGACGGTATCGGCCGCTACCAGTTGCTTGGCGAATCGGTGGACGATGCC 562
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                                                          LeuAlaLeuValGlnGlyValSerAspPheLeuLeuLeuGlyLysSerLeuAspIleAla
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Matches:
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILLING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILLING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILLING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 801
LENGTH: 1206
TYPE: DNA
                                                                       US-10-649-273-2_COPY_176_414 (1-239)
                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 801, Application US/09252991A Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: MARC J. RUBENFIELD et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS A
FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Pseudomonas aeruginosa
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LeuAlaLeuValGlnGlyValSerAspPheLeuLeuLeuGlyLysSerLeuAspIleAla
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49.54%
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18.63%
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                                                                                  x US-09-252-991A-801 (1-1206)
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RESULT 10
US-09-557-884-1/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/09557884
Patent NO. 6506581
GENERAL INFORMATION:
APPLICANT: Fleischmann et al.
APPLICANT: Fleischmann et al.
TITLE OF INVENTION: The Nucleotide sequence of the Haemophilus influenzae
Thereof, and Uses Thereof
              COMPUTER READABLE FORM:

MEDIUM TYPE: 3 1/2 inch diskette

COMPUTER: Dell Pentium

OPERATING SYSTEM: MS DOS v6.22

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/557,884

FILING DATE: 25-Apr-2000

CLASSIFICATION: -Unknown>

PEICM. APPLICATION UNMBER: 08/476,102

FILING DATE: JUN-5-1995

APPLICATION UNMBER: 08/476,102

FILING DATE: JUN-5-1995

APPLICATION UNMBER: 08/476,102
                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences,
STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1027
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                                                                                                                                                                                                                                                                                                                               STATE: MD
                                                                                                                                                                                                                                                                                                                                                  CITY: Rockville
                                                                                                                                                                                                                                                                                       ZIP: 20850
Michelle S. Marks
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                                                                                                                                                                    RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No.:
                                                                                  Sequence 1, Application US/09643990A Patent No. 6528289
GENERAL INFORMATION:
                                          APPLICANT: Robert D. Pleischmann
Mark D. Adams
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US-10-649-273-2_COPY_176_414 (1-239) x US-09-557-884-1 (1-1830121)
US-09-643-990A-1/c
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-557-884-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                        552467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      552572 AAAACATTTGCCGCAAATACAGTTAATCAAGCAATTÄÄÄAACGÄĞĞĞĞGAACTGÄTÄĞÄĞ
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                                                                   552311 TTTTGTACAGATAATGGTGCGATGATTGCTTACACAGGTTTTTTTACGTTTAAAAACAAGGT
                                                                                                                                                        552371 GAAACGCTTGCGCACTTAATGCAAAATTTAGGTGGCGAAGTGTTTTATCCTCAACCTCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION: TELEPHONE: 301-309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE DESCRIPTION: SEQ
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                                                                                            180 LeuCysThrAspAsnGlyIleMetIleAlaTrpAsnGlyIleGluArgLeuArgAlaGly 199
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TYPE: nucleic acid
                                                                                                                                                                                                                                                GAAACAGGCTATAAACGTTTAGTGATTGCGGGAGGGGTGAGCGCAAATAAAAAACTCCGA
                                                                                                                                                                                                                                                                          ProGlnAsnAsnAlaValLeuValAlaSerGlyGlyValAlaSerAsnPheTyrIleArg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTCACATTTCCACGTCCAATGACAGATCGTGCAGGCCTTGATTTTAGTTTTTCTGGTTTA 552573
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Hamilton O. Smith Owen White

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US-10-649-273-2_COPY_176_414 (1-239)
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Best Local Similarity:
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                                       552572
                                                                                                                                                                                            552680
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PB186P1C1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 08/487,429
FILING DATE: 1995-06-07
APPLICATION NUMBER: 08/426,787
FILING DATE: 1995-04-21
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: 3 1/2 inch diskette
COMPUTER: Dell Pentium
OPERATING SYSTEM: MS DOS v6.22
SOFTWARE: ASCII Text
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences,
STREET: 9410 Key West Avenue
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LENGTH: 1830121 base
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                                     AAAACATTTGCCGCAAATACAGTTAATCAAGCAATTAAAAACGAGGGCGAACTGATAGAG
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                                                                          GlnHisValThrAspLysIleIleMetLysLysGluLysGluGluGly-----IleGlu
                                                                                                                  TTCACATTTCCACGTCCAATGACAGATCGTGCAGGCCTTGATTTTAGTTTTTCTGGTTTA
                                                                                                                                           PheAspIleLysProProLeuHisHisAlaLysAsnCysAspPheSerPheThrGlyLeu
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TELEFAX: 310-309-8439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/643,990A
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The Nucleotide sequence of the Haemophilus influenzae
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GENEKAL ANTONIAMAN, BATTY S.

APPLICANT: Goldman, Barry S.

APPLICANT: Hinkle, Gregory J.

APPLICANT: Slater, Steven C.

APPLICANT: Wiegand, Roger C.

TITLE OF INVENTION: Myxococcus xanthus Genome Sec

FILE REFERENCE: 38-10(15849)B

CURRENT APPLICATION NUMBER: US/09/902,540

CURRENT FILING DATE: 2001-07-10

PRIOR APPLICATION NUMBER: 60/217,883

PRIOR FILING DATE: 2000-07-10

NUMBER OF SEQ ID NOS: 16825

SEQ ID NO 6612

LENGTH: 996
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Best Local Similarity:
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GlyGlnIleLeuSerSerAlaAlaAspIleAlaAlaThrValGlnHisThrMetAlaCys 120
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APPLICANT: Goldman, Barry S.

APPLICANT: Hinkle, Gregory J.

APPLICANT: Slater, Steven C.

APPLICANT: Wiegand, Roger C.

TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses The:

FILE REFERENCE: 38-10(15849)B

CURRENT APPLICATION NUMBER: US/09/902,540

CURRENT FILING DATE: 2001-07-10

PRIOR APPLICATION NUMBER: 60/217,883

PRIOR APPLICATION NUMBER: 60/217,883

PRIOR APPLICATION NUMBER: 5000-07-10

NUMBER OF SEQ ID NOS: 16825

SEQ ID NO 503

LENGTH: 2582
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                                                               GlyGlnIleLeuSerSerAlaAlaAspIleAlaAlaThrValGlnHisThrMetAlaCys 120
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                                                                                                                                             TTGAAG------ACGGCGGTGCTGCACCACGTGCAGAAGCACGGCGTGCCGCAG
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 2341
LENGTH: 1074
TYPE: DNA. Bootons Titabilia
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GENERAL INFORMATION:
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122 LeuValLysArgThrHisArgAlaIleLeuPheCysLysGlnArgAspLeuLeuProGln 141
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                                                                                GlnIleLeuSerSerAlaAlaAspIleAlaAlaThrValGlnHisThrMetAlaCysHis 121
                                                                                                                                                                                                                                   PheAspIleLysProProLeuHisHisAlaLysAsnCysAspPheSerPheThrGlyLeu 81
                                                                                                                                                                                                                                                                                                                                                                GCTGGTGAAGCATTTGATAAAACAGCCAAGCTATTGGGGGCTT---GATTATCCC-----
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                                                                                                                                     AAAACCTTTGCCGCTAATACTATTCGTCAAAACGATGATTCAGAG------
                                                                                                                                                                      GlnHisValThrAspLysIleIleMetLysLysGluLysGluGluGlyIleGluLysGly 101
                                                                                                                                                                                                                                                                                                                           SerThrMetSerGlyGlyLysAlaIleGluHisLeuAlaLysGlnGlyAsnArgPheHis 61
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¥	142	AsnAsnAlaValLeuValAlaSerGlyGlyValAlaSerAsnPheTyrIleArgArg 160
ਰਾ ਹ	823	ACAGGCTTTAAACGCTTAGTGATGGCTGGGGGGGCGTAAGTGCTAACCGTACTTTACGCGCC 882
Ϋ́	161	uGluIleLeuThrAsnAlaThrGlnCysThrL
਼ਰ ੋਂ	883	AAAATGGCGATGATAATGGAACAACTCGGAGGGGAAGTGTTTTATGCTCGCCCTGAGTTA 942
ਲੋਂ ਵੱ	181 943	CysThrAspAsnGlyIleMetIleAlaTrpAsnGlyIleGluArgLeuArgAlaGlyLeu 200
¥	201	GlYlleLeuHisAspIleGluGlYlleArgTyrGluProLysCysProLeu 217
ë י	003	GAGGGGCCTTTA
ESULT 15 IS-09-489- Sequence Patent N GENERAL APPLICA	5 9-039A-2 ce 2050, No. 661 L INFORM	050 Application US/ 0836 ATION: ary Breton et. a
		CID AND E FOR D /09/489 27
PRIOR APPL PRIOR FILLI NUMBER OF: SEQ ID NO 2 LENGTH: 1. TYPE: DNA ORGANISM: IS-09-489-039,	OF S	PRIOR APPLICATION NUMBER: US 60/117,747 PRIOR FILING DATE: 1999-01-29 PRIOR FILING DATE: 1999-01-29 NUMBER OF SEQ ID NOS: 14342 EQ ID NO 2050 LENGTH: 1032 TYPE: DNA ORGANISM: Klebsiella pneumoniae 09-489-039A-2050
lignment S red. No.: core: ercent Sim lest Local puery Match DB;	Score	nment Scores: 1.55e-17 Length: 1032 . No.: 205.00 Matches: 66 e: 205.00 Matches: 29 ent Similarity: 43.58% Conservative: 29 Local Similarity: 30.28% Mismatches: 93 y Match: 16.53% Indels: 30 y Match: 4 Gaps: 7
IS-10-649-	.273-	.2_COPY_176_414 (1-239) x US-09-489-039A-2050 (1-1032)
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ਲੇ ਤੋ	42 553	SerThrMetSerGlyGlyLyBAlalleGluHisLeuAlaLysGlnGlyAsnArgPheHis 61
ਲ ਲ	62 601	PheAspIleLysProProLeuHisHisAlaLysAsnCysAspPheSerPheThrGlyLeu 81
ਰ ਵ	82 661	GlnHisValThrAspLysIleIleMetLysLysGluLysGluGluGlyIleGluLysGly 101 ::: AAGACCTTCGCCGCCAACACCATTCGCAGCAACGGCGACGATGAG
¥	102	GlnIleLeuSerSerAlaAlaAspIleAlaAlaThrValGlnHisThrMetAlaCysHis 121
ŧ 6	706	, ,
-27	122	LeuValLysArgThrHisArgAlaIleLeuPheCysLysGlnArgAspLeuLeuProGln 141

Search completed: June 17, 2005, 02:30:33 Job time : 984.721 secs

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-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Maximum Match 100%
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Ygapop 10.0 , 1
Ygapop 6.0 ,
Fgapop 6.0 ,
Delop 6.0 ,
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/cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
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/cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
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n2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
n2_6/ptodata/1/pubpna/USO9A_PUBCOMB.seq:*
gn2_6/ptodata/1/pubpna/USO9B_PUBCOMB.seq:*
gn2_6/ptodata/1/pubpna/USO9C_PUBCOMB.seq:*
gn2_6/ptodata/1/pubpna/USO9C_PUBCOMB.seq:*
gn2_6/ptodata/1/pubpna/USO9C_PUBCOMB.seq:*
gn2_6/ptodata/1/pubpna/USOA_PUBCOMB.seq:*
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_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
_6/ptodata/1/pubpna/US10G_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

RBSULT 1 US-10-120-988-177 ; Sequence 177, Application		44 207.5 16.7 45 206 16.6	208 16.8	08 16.8	41 210 16.9	213 17.2	38 213 17.2	C 36 224 18.1 18	5 224 18.1	4 224 18.1	32 231 18.6	1 239 19.3	0 239 19.3	9 241 19.4	248.5 20.0 9	6 248.5 20.0	5 248.5 20.0	3 270 21.8 4 257 20.7	2 337 27.2	468	0 468 37.7	725 58.5	5 58.5 1	1059 85.4	1203 97.0	, 1203 97.	лù	3.5 97.	1213.5 97.	100.0	7 1240 100.0	1240 100.0	100.	0 100.	1 1240 100.0	Result Query No. Score Match Le
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US/10120988	ALIGNMENTS	US-10-282-122A-31809 US-09-815-242-6207	US-10-437-963-9	US-10-282-122A-	US-10-282-122A-	US-10-282-	US-09-815-242-96	17 US-10-329-670-1	US-10-282-122A-	9-815-242-69	US-U9-815-242-77016	-10-081-051-2	US-10-081-051-8	US-10-282-122A-31043	-10-672-7	S-10-282-122F	-10-343-56	US-10-43/-963-11249	8-10-424-59	-10-430-201-	US-10-651-722-20 US-10-430-201-3118	-10-649-273-	-10-067-443-20	US-10-094-749-400	-10-012-140-	-10-012-140-6	115-10-887-5533-1047	-10-649-27	-10-067-443-	-10-480-988-	US-10-651-722-1	-10-067-443	-10-651-722-	-10-649-273-	US-10-120-988-177	ID
		Sequence 6207, Ap	e 9137, A	e 19220,	977.	39301	9682,	sequence 1, Appli Sequence 1, Appli	e 2202	6946, Ap	Sequence //UI, Ap	e 2, App1	e 8, Appl	Sequence 31043, A	e 38,	e 2697	e 50, App	Semience 11249, A	e 66417,	e 311	Ť	20,	e 20, A	Sequence 400, App	4.	e 6	Ξ.	, 12	21,	36, App	Sequence 1, Appli	بر د	23,	e 23	Sequence 177, App Seguence 23, Appl	Description

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BSULT 1

$-10-120-988-177

Sequence 177, Application US/10120988

Publication No. US20030219745A1

GENERAL INFORMATION:

APPLICANT: Tang, Y. Tom

APPLICANT: Goodrich, Ryle

APPLICANT: Liu, Chenghua

APPLICANT: Hang, Dunrui

APPLICANT: Wang, Dunrui

APPLICANT: Drmanac, Radoje T.

TITLE OF INVENTION: No. US20030219745A1el Nucleic Acidc and ITLE REPERENCE: 802CON

CURRENT APPLICATION NUMBER: US/10/120,988

CURRENT FILING DATE: 2002-04-11
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; PRIOR APPLICATION NUMBER: 09/774,528; PRIOR FILING DATE: 2001-01-30; NUMBER OF SEQ ID NOS: 441; SOFTWARE: Pt FL_genes Version 2.0; SEQ ID NO 177; LENGTH: 1416; TYPE; DNA; ORGANISM: Homo sapiens; PEATURE: NAME/KEY: CDS; LOCATION: (205)...(1305)
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Pred. No.:
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                                   IleSerLysGluValGlyGluAlaSerIleLysValProGlnLeuLysMetGluIle
                                                                                                                                                                                                   AlaLeuGluIleLeuThrAsnAlaThrGlnCysThrLeuLeuCysProProProArgLeu 180
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                                                                                    GlyIleLeuHisAspIleGluGlyIleArgTyrGluProLysCysProLeuGlyValAsp 220
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Matches:
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Mismatches:
Indels:
Gaps:
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GENERAL INFORMATION:

APPLICANT: Bristol-Myers Squibb Company
ITITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A N
ITITLE OF INVENTION: SPINAL CORD, MP-1
FILE REFERENCE: D0073 NP
CURRENT APPLICATION NUMBER: US/10/067,443
CURRENT FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR APPLICATION NUMBER: US 60/264,518
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR APPLICATION NUMBER: US 60/282,814
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Publication No. US20030082782A1
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TYPE: DNA
ORGANISM: homo s
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                                                  GCTCTGGAAATTTTAACAAACGCAACACAGTGCACTTTGTTGTGTCCTCCTCCCAGACTA
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Sequence 23, Application US/10649273

Publication No. US20040043407A1

GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
ITILE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE, MP-1

FILE REFERENCE: D0073 CNT
CURRENT APPLICATION NUMBER: US/10/649,273

CURRENT FILING DATE: 2003-08-27

PRIOR APPLICATION NUMBER: US 60/266,518

PRIOR APPLICATION NUMBER: US 00/67,443

PRIOR APPLICATION NUMBER: US 10/067,443

PRIOR APPLICATION NUMBER: US 00/67,443

PRIOR FILING DATE: 2001-02-05

PRIOR FILING DATE: 2001-04-10

NUMBER OF SEQ ID NOS: 71

SOFTWARE: PatentIn version 3.2

SOFTWARE: PatentIn version 3.2
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TYPE: DNA
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AlaLeuGluIleLeuThrAsnAlaThrGlnCysThrLeuLeuCysProProProArgLeu 180
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US-10-651-722-23
Sequence 23, Application US/10651722
Publication No. US20040048302A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING
FILE REFERENCE: D0073 DIV
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CURRENT FILING DATE: 2003-08-29
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 10/067,443
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SOFTWARE: Patentin version 3.2
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LENGTH: 1526
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SQ ID NO 1
LENGTH: 2197
TYPE: DNA
ORGANISM: Homo sapiens
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Publication No. US20030082782A1
GENERAL INFORMATION:
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TITLE OF INVENTION: POLYNUCLECTINE ENCODING A NOVEL METALOPROTEASE HIGHLY EXPRESSED
TITLE OF INVENTION: SPINAL CORD, MP-1
PILE REFERENCE: D0073 NP
CURRENT APPLICATION NUMBER: US/10/667,443
CURRENT FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: CDS
LOCATION: (231)..(1472)
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                                                                                                    AlaProGlyAspMetLeuAspLysValAlaArgArgLeuSerLeuIleLysHisProGlu 40
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                                               CysSerThrMetSerGlyGlyLysAlaIleGluHisLeuAlaLysGlnGlyAsnArgPhe 60
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 HisPheAspIleLysProProLeuHisHisAlaLysAsnCysAspPheSerPheThrGly
                             TGCTCCACCATGAGTGGTGGGAAAGCCATAGAACATTTGGCCAAACAAGGAAATAGATTT 935
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Matches:
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APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A N
FILE REFERENCE: D0073 CNT
CURRENT APPLICATION NUMBER: US/10/649,273
CURRENT FILING DATE: 2003-08-27
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 10/067,443
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2002-05
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SOPTWARE: PATENTIN VERSION 3.2
LENGTH: 2197
                                                                                Percent Similarity:
Best Local Similarity:
Query Match:
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US-10-649-273-1
                         US-10-649-273-2_COPY_176_414 (1-239) x US-10-649-273-1 (1-2197)
                                                                                                                                       Score:
                                                                                                                                                                          Alignment Scores:
                                                                                                                                                                                                           US-10-649-273-1
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                                                                                                                                                                                                                                          FEATURE:
NAME/KEY: CDS
                                                                                                                                                                                                                                                                               ORGANISM: Homo
                                                                                                                                                                                                                              LOCATION: (231)..(1472)
                                                                                                                                                                                                                                                                                                TYPE: DNA
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Conservative:
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LeuLeuAlaLeuValGlnGlyValSerAspPheLeuLeuGlyLysSerLeuAspIle

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Sequence 1, Application US/10651722
; Sequence 1, Application US/20040048302A1
; GENERAL INFORMATION:
APPLICANT: BEISEOL-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE, MP-1
FILE REFERENCE: D0073 DIV
; CURRENT APPLICATION NUMBER: US/10/651,722
; CURRENT APPLICATION NUMBER: US/60/266,518
; PRIOR APPLICATION NUMBER: US 60/266,518
; PRIOR APPLICATION NUMBER: US 10/067,443
; PRIOR APPLICATION NUMBER: US 10/067,443
; PRIOR APPLICATION NUMBER: US 10/067,443
; PRIOR FILLING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: US 60/282,814
; PRIOR FILLING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
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US-10-651-722-1
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   FEATURE:
NAME/KEY: CDS
LOCATION: (231)..(1472)
-10-651-722-1
                                                              TYPE: DNA
ORGANISM: Homo sapiens
                                                                                           LENGTH: 2197
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Sequence 36, Application US/10480988

Publication No. US20050069877A1

GENERAL INFORMATION:
APPLICANT: GANDHI, Ameena R.; KABLE, Amy B.;
APPLICANT: SWARNAKAR, Anita: HAFALIA, April J.A.;
APPLICANT: TRAN, Bao; DUGGAN, Brendan M.;
APPLICANT: HARREN, Bridget A.; ISON, Craig H.;
APPLICANT: HONCHRIL, Cynthia D.; NGUYEN, Danniel B.;
APPLICANT: UJ, Dyung Aina M.; LEE, Ernestine A.;
APPLICANT: VUE, Henry; FORSYTHE, Ian J.;
APPLICANT: YUE, Henry; FORSYTHE, Ian J.;
APPLICANT: GRIFFIN, Jennifer A.; LI, Joana X.;
APPLICANT: GRIFFIN, Jennifer A.; LI, Joana X.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
Query Match:
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CURRENT FILING DATE: 2003-12-16
PRIOR APPLICATION NUMBER: PCT/USO2/19360
PRIOR FILING DATE: 2002-06-18
PRIOR APPLICATION NUMBER: US 60/300,508
PRIOR FILING DATE: 2001-06-22
PRIOR APPLICATION NUMBER: US 60/303,445
PRIOR APPLICATION NUMBER: US 60/303,445
PRIOR APPLICATION NUMBER: US 60/305,405
PRIOR APPLICATION NUMBER: US 60/305,405
PRIOR APPLICATION NUMBER: US 60/301,442
PRIOR APPLICATION NUMBER: US 60/311,442
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SOFTWARE: PERL Program
SEQ ID NO 36
LENGTH: 2572
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APPLICANT: GIETZEN, Kimberly J.; DING, Li;
APPLICANT: BAUGHN, Mariah R.; BOROWSKY, Mark L.;
APPLICANT: BAUGHN, Mariah R.; BOROWSKY, Mark C.;
APPLICANT: YAO, Monique G.; CHAWLA, Narinder K.;
APPLICANT: LEE, Sally; BECHA, Shanya D.;
APPLICANT: LEE, Sally; BECHA, Shanya D.;
APPLICANT: LEE, Soo Yeun; TRAN, Uyen K.;
APPLICANT: ELLIOTT, Vicki S.; LUO, Wen;
APPLICANT: LU, Yan; ZEBARJADIAN, Yeganeh
TITLE OF INVENTION: PROTEIN MODIFICATION AND MAINTENANCE MOLECULES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: US 60/314,821
PRIOR FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/315,992
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OTHER INFORMATION: Incyte ID
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APPLICATION NUMBER: US
FILING DATE: 2002-05-03
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GlyGlnIleLeuSerSerAlaAlaAspIleAlaAlaThrValGlnHisThrMetAlaCys
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Percent Similarity:
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Query Match:
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; ORGANISM: homo
US-10-067-443-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
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CURRENT APPLICATION NUMBER: US/10/067,443
CURRENT APPLICATION NUMBER: US/2-05
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 21, Application US/10067443 Publication No. US20030082782A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn version 3.0 SEQ ID NO 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Bristol-Myers Squibb Company TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING TITLE OF INVENTION: SPINAL CORD, MP-1
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HisPheAspIleLysProProLeuHisHisAlaLysAsnCysAspPheSerPheThrGly
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Publication No. US20040043407A1

GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING
FILE REFERENCE: DO073 CNT
CURRENT APPLICATION NUMBER: US/10/649,273
CURRENT FILING DATE: 2003-08-27
CURRENT FILING DATE: 2003-08-27
                                                                                                                                                                                                       SEQ ID NO 21
                                                                                                                                                                                                                                  PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 10/067,443
PRIOR FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
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                                                                                                                                                                                                       RESULT 11
US-10-651-722-21
                                                                                                 Sequence 21, Application US/10651722
publication No. US20040048302A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING
FILE REFERENCE: D0073 DIV
 CURRENT APPLICATION NUMBER: US/10/651,722
CURRENT FILING DATE: 2003-08-29
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 10/067,443
PRIOR FILING DATE: 2002-02-05
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PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
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LysMetGluIle 239
                                             ProLeuGlyValAspIleSerLysGluValGlyGluAlaSerIleLysValProGlnLeu
                                                                                        CTACGTGGTGGCTTGGGCATTTTACATGACATAGAAGGCATCCGCTATGAACCAAAATGT
                                                                                                                                                      CCTCCTCCCAGACTATGCACTGATAATGGCATTATGATTGCATGGAATGGTATTGAAAGA
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                            CCTCTTGGAGTAGACATATCAAAAGAAGTTGGAGAAGCTTCCATAAAAGTACCACAATTA
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Query Match:
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SEQ ID NO 1047
LENGTH: 1387
TYPE: DNA
ORGANISM: human
US-10-887-553A-1047
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CURRENT APPLICATION NUMBER: US/10/887,553A
CURRENT FILING DATE: 2004-07-08
PRIOR APPLICATION NUMBER: 60/485,883
PRIOR FILING DATE: 2003-08-07
NUMBER OF SEQ ID NOS: 1208
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APPLICANT: Li, Hao
TITLE OF INVENTION: Method to treat conditions associated
TITLE OF INVENTION: with insulin signalling dysregulation
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PheTyrIleArgArgAlaLeuGluIleLeuThrAsnAlaThrGlnCysThrLeuLeuCys 175
                                                      ArgAspLeuLeuProGlnAsnAsnAlaValLeuValAlaSerGlyGlyValAlaSerAsn 155
                                                                                                                                               HisThrMetÄlaCysHisLeuValLysArgThrHisArgAlaIleLeuPheCysLysGln 135
                                                                                                                                                                                                                                                                     ATTAGTAAAGTTGAACAGATAAATATTCCTGGATTGTGCCTAAAAAATAGCTGCTCATTTC 908
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APPLICANT: Kapeller-Libermann, Rosana
APPLICANT: Kapeller-Libermann, Rosana
APPLICANT: Glucksmann, Maria A.
APPLICANT: Glucksmann, Maria A.
APPLICANT: Glucksmann, Maria A.
APPLICANT: Glucksmann, Maria A.
APPLICANT: Blocksmann, Maria A.
APPLICANTON: 14354 METHODS AND COMPO
TITLE OF INVENTION: 14354 METHODS AND COMPO
TITLE OF INVENTION: 14354 METHODS AND COMPO
TITLE REFERENCE: 381552004900
CURRENT APPLICATION NUMBER: US/10/012,140
CURRENT FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: 60/246,768
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-08
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PRIOR FILING DATE: 2000-11-16
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APPLICANT: Leiby, Kevin R.
APPLICANT: Kapeller-Libermann, Rosana
APPLICANT: Glucksmann, Maria A.
TITLE OF INVENTION: 38650, 28472, 5495, 65507, 81588, AND
TITLE OF INVENTION: 14354 METHODS AND COMPOSITIONS OF HUMAN PROTEINS AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 381523004900
CURRENT APPLICATION NUMBER: US/10/012,140
CURRENT FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: 60/246,768
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: 60/246,772
PRIOR APPLICATION NUMBER: 60/246,772
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-08
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PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-15
NUMBER OF SEQ ID NOS: 49
                                                  Percent Similarity:
Best Local Similarity:
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US-10-012-140-4
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                                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: (1)...(1820)
OTHER INFORMATION: n = A,T,C
                                                                                                                                                                                                                                                                                                                NAME/KEY: CDS
LOCATION: (146)...(1390)
FEATURE:
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ORGANISM: Homo
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RESULT 15
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Publication No: US200
GENERAL INFORMATION:
APPLICANT: ISOGAI, T
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OTSUKA, KAORU
NAGAI, KEIICHI
IRIE, RYOTARO
TAMECHIKA, ICHIRO
SEKI, NAOHIKO
YOSHIKAMA, TSUTOMU
OTSUKA, MOTOYUKI
NAGAHARI, KENJI
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OTSUKI, TETSUJI
WAKAMATSU, AI
SATO, HIROYUKI
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YAMAMOTO, JUN-ICHI
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b: US20030219741A1
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Best Local Similarity:
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TITLE OF INVENTION: NOVEL PULL-LENGTH CDNA
FILE REFERENCE: 084335/0160
CURRENT APPLICATION NUMBER: US/10/094,749
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 60/350,435
PRIOR FILING DATE: 2002-01-24
PRIOR PILING DATE: 2001-09-14
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 3381
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SEQ ID NO 400
LENGTH: 2208
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   IleSerLysGluValGlyGluAlaSerIleLysValProGlnLeuLysMetGluIle
                                                                   GlyIleLeuHisAspIleGluGlyIleArgTyrGluProLysCysProLeuGlyValAsp
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Search completed: June 17, 2005, 08:03:30 Job time : 1634.64 secs

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Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlp
-Q=/cgn2 1/USPTO_spool_p/US10649273/runat 15062005_111417_6057/app_query.fasta_1.1429
-Q=-/cgn2 1/USPTO_spool_p/US10649273/runat 15062005_111417_6057/app_query.fasta_1.1429
-DB=Issued_patents_NA -QFMT=fastap -SUPFIX=p2n.rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=Dits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
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-USER=US10649273 @CGN 1 1.77 @runat 15062005 111417 6057 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQÜERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

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4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

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Sequence 806, Appl
Sequence 801, App
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Sequence 2341, Ap
Sequence 6612, Ap
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                           ThrHisArgAlaIleLeuPheCysLysGlnArgAspLeuLeuProGlnAsnAsnAlaVal
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                                                                                    CTGGTTGCATCTGGTGGTGTCGCAAGTAACTTCTATATCCGCAGAGCTCTGGAAATTTTA
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Sequence 21, Application US/10067443

Patent No. 6642041

GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A I
TITLE OF INVENTION: SPINAL CORD, MP-1

FILE REFERENCE: D0073 NP
CURRENT APPLICATION NUMBER: US/10/067,443

CURRENT FILING DATE: 2002-02-05

PRIOR APPLICATION NUMBER: US 60/266,518

PRIOR PILING DATE: 2001-02-05

PRIOR APPLICATION NUMBER: US 60/282,814

PRIOR APPLICATION NUMBER: US 60/282,814

PRIOR FILING DATE: 2001-04-10

NUMBER OF SEQ ID NOS: 71
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Query Match:
DB:
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US-10-067-443-21
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US-10-067-443-21
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SEQ ID NO 21
LENGTH: 1387
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TYPE: DNA
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ProPheIleProIleHisHisMetGluAlaHisAlaLeuThrIleArgLeuThrAsnLys
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Sequence 177, Application US/09774528
Patent No. 6743619
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Zhou, Ping
APPLICANT: Zhou, Ping
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Asundi, Vinod
APPLICANT: Ann, reiyan
APPLICANT: Zhang, Jie
APPLICANT: Zhao, Qing A.
APPLICANT: Yang, Yonghong
                                                                                                                                            RESULT 3
US-09-774-528-177
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APPLICANT: Dranac, Radoje T.
TITLE OF INVENTION: No. 6743619el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 802
CURRENT FILING BATE: 2001-01-30
NUMBER OF SEQ ID NOS: 441
SOFTWARE: pt_FL_genes Version 2.0
SEQ ID NO 177
LENGTH: 1416
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (205)...(1305)
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APPLICANT:
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Wehrman, Tom
Wang, Jian-Rui
Wang, Dunrui
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                                     ThrGlyLeuGlnHisValThrAspLysIleIleMetLysLysGluLysGluGluGlyIle
                                                                                   LeuValGlyGlnLeuLysLysProPheIleProIleHisHisMetGluAlaHisAlaLeu
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Matches:
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US-10-067-443-23
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                                                                                                                                                                                                                                                                                                                                     ; TYPE: DNA
; ORGANISM: homo
US-10-067-443-23
                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: D0073 NP
CURRENT APPLICATION NUMBER: US/10/067,443
CURRENT FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SOFTWARE: PatentIn version 3.0
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Best Local Similarity:
                                                                                                                                                                                                                                                                                       Alignment Scores
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 23, Applicate Patent No. 6642041
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Bristol-Myers Squibb Company TITLE OF INVENTION: POLYNUCLBOTIDE ENCODING TITLE OF INVENTION: SPINAL CORD, MP-1
                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 1526
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188 LeuLeuGlyLysSerLeuAspIleAlaProGlyAspMetLeuAspLysValAlaArgArg
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 Percent Similarity:
                                  Pred. No.:
                                                                                US-10-067-443-20
                                                                                                                                                                      PATENT NO. 6642041

GENERAL INFORMATION:

APPLICANT: Bristol-Myers Squibb Company

TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE HIGHLY EXPRESSED

TITLE OF INVENTION: SPINAL CORD, MP-1

FILE REFERENCE: D0073 NP

CURRENT APPLICATION NUMBER: US/10/067,443

CURRENT FILING DATE: 2002-02-05

PRIOR APPLICATION NUMBER: US 60/266,518

PRIOR APPLICATION NUMBER: US 60/266,518

PRIOR APPLICATION NUMBER: US 60/266,518

PRIOR APPLICATION NUMBER: US 60/282,814

PRIOR PILING DATE: 2001-04-10

NUMBER OF SEQ ID NOS: 71

NUMBER OF SEQ ID NOS: 71
                                                                                                                                           SOFTWARE: Pa
                                                                                                                                                                                                                                                                                                                                                                  Sequence 20, Application US/10067443 Patent No. 6642041
                                                                                                               TYPE:
                                                                                              TYPE: DNA
ORGANISM: homo
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Db 11582 TCAAGCCCATTTTCCAACCAATAGAAGAGCAAACATAGACAGGGGCAGTGATTGGCCTCT 11641		204	· 11462 GCCATATATAGGAAAACAAACAAACAAACAAACACTGCTTCCCACAGTGAAATAA	Qy 204 204	Db 11402 TACACCACAGACAGGGTCCCCCCCCCCCCCCTTTGTTTTAGAATACTACAGAGGCTACT 11461	Qy 204 204	Db 11342 ATATAGATTAACATAAGGACATTAAAGATGCAATGCACAGAATTAAATCACACAATTACT 11401	Оу 204 204	11	Db 11222 ATCTGTACATAAAGGCTGAAATAGTTTGCAGATAAGGTTATGTATTTTGCCAAATAATGT 11281 Oy 204 204		Db 11162 AAGAGTAGTACACAATTTTATAATTCTTAGCCTTTCTTAATAAAATGGTAAGAGGTTCAT 11221	Qy 204 204	Db 11102 TATTTCTGAATTTTATCTTAGTAAACTGAAAAAATTCACATATGGTGAGAAAAATAGA 11161	Qy 204 204	Db 11042 TTTGTTATGTTGTCCATTTCAACTAAGTAGCAATAGATGTGCTACCACCATTCACCTAAA 11101	Qy 204 204	Db 10983 GACATAGCACCAGGTGACATGCTTGACAAGGT-AATTAAGAATTAATTTCTCCATTCTTT 11041	Qy 194 AspIleAlaProGlyAspMetLeuAspLysVal 204 ,	Db 10923 CACTGTCTGTCGCATTAGTTCAAGGAGTTTCAGATTTTCTGCTTCATGAAAGTCTTTG 10982	TOOD WINITHMOTICHACHAIRMANTACHAMATICHTITITAGITATICHTICAGATACHT	154 ThrileArgLeuThrAsnLysValGluPheProPheLeuValLeuLeuIleSerGlyGly 173	Db 10803 CTGGTAGGACAGTTAAAAAAGCCATTCATTCATCATCATCATCATGGAGGCTCATGCACTT 10862	Qy 134 LeuValGlyGlnLeuLysLysProPheIleProIleHisHisMetGluAlaHisAlaLeu 153	10743 ACTACCATAAAACCAGGACTTGCTTTAAGCCTGGGAGTGGGCTTATCATTTAGCTTACAG	114 ThrThrIleLvsProGlvLeuAlaLeuSerLeuGlvValGlvLeuSerPheSerLeuGln	Oy 94 IleValGluGluAlaLeuSerAlaSerGlyValSerProSerAspLeuSerAlaILeAla 113	10623 AGAACAGGTGGGATTGTTCCTCCAGCAGCTCAACAGCTTCACAGAGAAAATATTCAACGA	Qy 74 LysThrGlyGlyIleValProProAlaAlaGlnGlnLeuHisArgGluAsnIleGlnArg 93	US-10-649-273-2 (1-414) x US-10-067-443-20 (1-14364)	Best Local Similarity: 32.20% Mismatches: 2 Query Match: 55.84% Indels: 657 DB: 4 Gaps: 4
Db 12662 TCCAACTTTCGTGACACTAATGTTGATAAAGTTCTGATAATCCACTATATTGTACCAGCC 12721	Qy 321 321	Db 12602 ATCCCTTTGTTTGTTTGTTTTTTAATAAGCCAGTCAAATTTAGCAGTGGGAGGTGGTAT 12661	Qy 321 321	12	321	12482 AGTCTAATTTTGCATCTTCTTGTTGGATTTAAAAGAGGGCTTACAATAAAGAAAG		QY 321	12362 CTTTATGCCTTATGCTAGCCCTGACAGTATGAAATTATGCAGGATAGGAAAGACTAACAG		Db 12302 CACTTTGCAATATGTTACTTTTTTCCCAAGACCTTGACCTTGTGTTTAGGATGAACAGAT 12361	321	12242 CTTGTTACCTCAAAATAATGCAGTACTGGTAAGTTTTATCTCATTTTATAGTAATAGTTA	312 pLeuLeuProGlnAsnAsnAlaValleu312 pLeuLeuProGlnAsnAsnAlaValleu	Db 12182 AATGGCATGTCATCTTGTGAAAAGAACACATCGGGCTATTCTGTTAAGCAGAGAGA 12241	2012 - 1411 TOTACH COLONIA TOTACH COLONIA COLO	74792098741798743735174747474747474747474747474747474747474	T2067 AAACITIAAACAGATAAAATATICCIKSSTASSASSASSASSASSASSASSASSASSASSASSASSA	OF 12062 BARGETGABACAGATABABATATTCCTGGATTGGCTABABABTAGCTGCTGATTTCTGCBGG	12002 CACGTTACTGATAAAATAATAATGAAAAAGGGAAAAGGGAAAGGTATATTTCTAATTA	Qy 258 HisValThrAspLysIleIleMetLysGysGluCysGluGlu 271	11942 GACATCAAACCTCCCTTGCATCATGCTAAAAATTGTGATTTTCTTTTACTGGACTTCAA	238 AspIleLysProProLeuHisHisAlaLysAsnCysAspPheSerPheThrGlyLeuGln	Oy 218 TITTEATHER THE TOTAL AND THE TOTAL AN	11822 AATATGTTTCTTTGATAGGTGĞĊĀĀĞĀĀĞĀČTTTCTTTĀĀTĀĀĀĀĀČĀTCCĀĞĀĞTGCTCC			Оу 204 204	11		

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APPLICANT: Lagace, Robert, E.
APPLICANT: Patterson, Chandra
APPLICANT: Berg, Kim, L.
TITLS OF INVENTION: NUCLEOTIDE SEQUENCES OF
FILE REFERENCE: PM-0008-4 US
CURRENT APPLICATION NUMBER: US/09/596,002
CURRENT FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: 60/140,121
PRIOR FILING DATE: 1999-06-18
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     SEQ
                                                                                                                                                                                                                     Patent No. 6632636 GENERAL INFORMATION:
                                                                                                                                                                                                                                        Sequence 38, Application US/09596002 Patent No. 6632636
   SOFTWARE:
EQ ID NO 38
                                      NUMBER OF SEQ ID NOS:
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                                                                                                                                                                                                                                                                                                                                                    isAspIleGluGlyIleArgTyrGluProLys 389
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Best Local Similarity:
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OTHER INFORMATION: Incyte template
PUBLICATION INFORMATION:
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TYPE: DNA
ORGANISM: M. catarrhalis
FEATURE:
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LysHisProGluCysSerThrMetSerGlyGlyLysAlaIleGluHisLeuAlaLysGln
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TATACCAAAGGGCCAGGGCTGATTGGGGCGTTGATGACAGGGGCATTATTTGGGCCGGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ThrThrIleLysProGlyLeuAlaLeuSerLeuGlyValGlyLeuSerPheSerLeuGln 133
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                                                       AGCGACCCC
                                                                                          GlyIleGluLysGlyGlnIleLeuSerSerAlaAlaAspIleAlaAlaThrValGlnHis 291
                                                                                                                       TCGTTCAGTGGCATGAAAACCGCCATTCATAATCTCATCATAAGACACACCAAACGCCCAA
                                                                                                                                                            SerPheThrGlyLeuGlnHisValThrAspLysIleIleMetLysLysGluLysGluGlu
                                                                                                                                                                                                   GGCAACCCACACGCCTATGAGCTGCCAAGACCCCATGCAGCAT---AAAGGGCTGGATTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                   GGCGGTCATACCATGCTGCGTGCCGATGGTGTGGGCGTGTATCAGATATTGGGCGAG
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                                                                                                                                                                                                                                                                                                                                             TCTATCGATGATGCGGTGGGTGAATGCTTTGATAAAACGGCAAAAATGCTCAAACTG---
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Percent Similarity:
Best Local Similarity:
Query Match:
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PATENT NO. 6673910
GENERAL INFORMATION:
APPLICANT: GATY L. Breton et al.
APPLICANT: GATY L. Breton et al.
APPLICANT: OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARTITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 2709.2005-001
CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT FILING DATE: 2000-04-04
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SEQ ID NO 806
LENGTH: 1053
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316 GCGTATGGGCTGGGCGTGCCAGCGGTTGGGGTGCATCATATGGAGGGACATCTGTTAGCA 375
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16 GTATTGGGATTGGAGACATCTTGTGATGATACAGGGCTTGCCATCTATGATAGTACGATG 75
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                        ValGlyGlnLeuLysLysProPheIleProIleHisHisMetGluAlaHisAlaLeuThr 154
                                                                                                                                                                        TTTAATGAGATGTTGGATCAGGCAAATATCACCAAATCCGACATTGATGCGGTGGCGTAT 255
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                                                                                                                                                                                                                                                                                                                                                                                        ------GlyAsnValLeuGlyGluAlaIleHisSerGlnThrGluValHisLeuLys 74
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GENERAL INFORMATION:
                                                                  SEQ ID NO 801
                                                                                 CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEO ID NOS: 33142
                                                                                                                                                                                                                                    APPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                        LENGTH: 12
TYPE: DNA
    ORGANISM: Pseudomonas aeruginosa
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Alignment Scores: Pred. No.: Score:
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                                                                       US-09-543-681A-2341
                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: GARY BREYON
APPLICANT: GARY BREYON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR PILING DATE: 1999-04-09
PRIOR FILING DATE: 1999-04-09
                                                                                                                      NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 2341
LENGTH: 1074
                                                                                                                                                                                                                                                                                                                                         Sequence 2341, Application Patent No. 6605709
                                                                                       ORGANISM: Proteus
                                                                                                        TYPE: DNA
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 ThraspasnGlyIleMetIleAlaTrpAsnGlyIleGluArgLeuArgAlaGlyLeu---
                                                                                                                                              Asn---AlaValLeuValAlaSerGlyGlyValAlaSerAsnPheTyrIleArgArgAla 336
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                                                                                       LeuGluIleLeuThrAsnAlaThrGlnCysThrLeuLeuCysProProProArgLeuCys 356
                                                                                                                              GGCTTTAAACGCTTAGTGATGGCTGGGGGGCGTAAGTGCTAACCGTACTTTACGCGCCCAAA 885
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APPLICANT: Hinkle, Gregory J.

APPLICANT: Slater, Steven C.

APPLICANT: Wiegand, Roger C.

ITITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses
FILE REFERENCE: 38-10(15849)B

CURRENT APPLICATION NUMBER: US/09/902,540

CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10

SEQ. ID NO 6612

LENGTH: 996

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Patent No. 6833447
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                            ProGlyAspMetLeuAspLysValAlaArgArgLeuSerLeuIleLysHisProGluCys 216
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; ORGANISM: Myxococcus xanthus
US-09-902-540-503
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APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Service Ser
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Sequence 1, Application US/08087797 Patent No. 5543312 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTCTACGAGGTGCAGGCCTACGGGCAGTACCGGCTGGTGGTGGCAGCACGCGCGACGACGCG 1046
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
Best Local Similarity:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: ETITLE OF INVENTION: GTITLE OF INVENTION: GUIDNER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
APPLICANT:
APPLICANT:
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NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/087,797
FILING DATE: 114-JUL-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 1315 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: 704 377 1561
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Layton, Jr., Samuel G.
REGISTRATION NUMBER: 22807
REFERENCE/DOCKET NUMBER: 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 1211 East Morehead St
CITY: Charlotte
STATE: No. 5543312th Carolina
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ZIP: 28234
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STREET: 1211 East Morehead
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      296 CCGTAAAACGTTGCCACTAATTCAAGAAGCCTTAAAAGAGGCCCAATCTGCAACCCTCGGA
                                                                                                                                                                  176 AACCGGTGTTGCCATTTATGATGAAGACAAAGGCTTAGTGGCAAACCAGCTTTATAGCCA
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                                                                                   nThrGluValHisLeuLysThrGlyGlyIleValProProAlaAlaGlnGlnLeuHisAr 88
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                                           gGluAsnIleGlnArgIleValGlnGluAlaLeuSerAlaSerGlyValSerProSerAs 108
                                                                                                                                                                                                          pThrAlaAlaAlaValValAspGluThrGlyAsnValLeuGlyGluAlaIleHisSerGl
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Lo, Reggie Y.C.
Abdullah, Khalid M.
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SULT 14
3-09-557-884-1/c
Sequence 1, Application US/09557884
Sequence 10. 6506581
Patent No. 6506581
Patent INFORMATION:
APPLICANT: Fleischmann et al.
TITLE OF INVENTION: The Nucleotide sequence of Title of Invention and Uses Thereof
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences,
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: MD
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                     1082
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Best Local Similarity:
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/557,884
PILING DATE: 25-Apr-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/476,102
PILING DATE: JUN-5-1995
ATTORNEY/AGENT INFORMATION:
NAME: Michelle S. Marks
REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PB186P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3 1/2 inch diskette
COMPUTER: Dell Pentium
COMPUTER: Mell Pentium
OPERATING SYSTEM: MS DOS v6.22
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE DESCRIPTION: SEQ
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GlyAspMetLeuAspLysValAlaArgArgLeuSerLeuIleLysHisProGluCysSer 217
                                                                                                                                                  GACAATTCACCGCACTTTCCTTTTGTTGCTCTGTTGGTATCGGGTGGCCACACTCAATTA
                                                                                                                                                                                                                                     AATGITCCTGCGATTGGTGTTCATCATATGGAAGGGCATTTACTTGCGCCAATGCTTGAT 552849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AsnValLeuGlyGluAlaIleHisSerGlnThrGluValHisLeuLysThrGlyGlyIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                               GTGCGTGTCGATGGTAGGAAAATATGAAGTGATAGGAGAATCTATTGATGATGCTGCT 552729
                                                                                                  AlaLeuValGlnGlyValSerAspPheLeuLeuLeuGlyLysSerLeuAspIleAlaPro
                                                                                                                                                                                         ThrAsnLysValGluPheProPheLeuValLeuLeuIleSerGlyGlyHisCysLeuLeu 177
                                                                                                                                                                                                                                                                              LysLysProPheIleProIleHisHisMetGluAlaHisAlaLeuThrIleArgLeu---
                                                                                                                                                                                                                                                                                                                          GGGCTTGTTGGCGCATTGCTTGTCGGTGCTACGATTGCACGTTCTTTAGCCTATGCTTTGG 552909
                                                                                                                                                                                                                                                                                                                                                               GlyLeuAlaLeuSerLeuGlyValGlyLeuSerPheSerLeuGlnLeuValGlyGlnLeu 138
                                                                                                                                                                                                                                                                                                                                                                                                             TTAGAGGAAGCCAATTTAACCGCGAGCGATATTGATGGTATTGCTTATACGAGTGGCCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                  LeuSerAlaSerGlyValSerProSerAspLeuSerAlaIleAlaThrThrIleLysPro 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTTCCTGAATTAGCATCACGTGATCATATTCGGAAAACAGCACCTCTTATTAAAGCGGCA
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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RESULT 15
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         552728 GGCGAAGCCTTTGATAAAACAGCAAAATTACTTGGACTA---GATTATCCA-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    552368 ACGCTTGCGCACTTAATGCAAAATTTAGGTGGCGAAGTGTTTTATCCTCAACCTCAATTT 552309
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                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: 3 1/2 inch diskette
COMPUTER: Dell Pentium
OPERATING SYSTEM: MS DOS v6.22
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                              APPLICATION NUMBER: US/09/643,990A
PILING DATE: 23-Aug-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE Human Genome Scien
STREET: 9410 Key West Avenue
                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Robert D. Fleischmann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GlnAsnAsnAlaValLeuValAlaSerGlyGlyValAlaSerAsnPheTyrIleArgArg 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACATTTGCCGCAAATACAGTTAATCAAGCAATTAAAAACGAGGGGGGAACTGATAGAGCAA 552510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HisLeuValLysArgThrHisArgAlaIleLeuPheCysLysGlnArgAspLeuLeuPro 315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CysThrAspAsnGlyIleMetIleAlaTrpAsnGlyIleGluArgLeuArgAlaGly 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AlaLeuGluIleLeuThrAsnAlaThrGlnCysThrLeuLeuCysProProProArgLeu 355
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                                                                                                                                                                                                                                                                                                                                                                                                             STATE: MD
                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Rockville,
NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PB
                                                                               APPLICATION NUMBER: 08/426,787
FILING DATE: 1995-04-21
                                                                                                                      APPLICATION NUMBER: 08/487,429 FILING DATE: 1995-06-07
                                                                                                                                                                                                                                                                                                                                                                      ZIP: 20850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. Craig Venter
J. Craig Venter
INVENTION: The Nucleotide sequence of inventions influenzae
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Owen White
Hamilton O. Smith
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genome Sciences,
    PB186P1C1
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SEQUENCE DESCRIPTION: SEQ
US-09-643-990A-1
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        552509
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LENGTH: 1830121 base
TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ThrMetSerGlyGlyLysAlaIleGluHisLeuAlaLysGlnGlyAsnArgPheHisPhe 237
                                                                                                                                                                                                                                                                                                                                                                   GlyAspMetLeuAspLysValAlaArgArgLeuSerLeuIleLysHisProGluCysSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GACAATTCACCGCACTTTCCTTTTGTTGCTCTGTTGGTATCGGGTGGCCACACTCAATTA 552789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ThrAsnLysValGluPheProPheLeuValLeuIleSerGlyGlyHisCysLeuLeu 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LysLysProPheIleProIleHisHisMetGluAlaHisAlaLeuThrIleArgLeu--- 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGGCTTGTTGGCGCATTGCTTGTCGGTGCTACGATTGCACGTTCTTTAGCCTATGCTTGG 552909
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AsnValLeuGlyGluAlaIleHisSerGlnThrGluValHisLeuLysThrGlyGlyIle 78
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                                             GlyGlnIleLeuSerSerAlaAlaAspIleAlaAlaThrValGlnHisThrMetAlaCys
                                                                                     ACATTTGCCGCAAATACAGTTAATCAAGCAATTAAAAACGAGGGGGAACTGATAGAGCAA
                                                                                                          HisValThrAspLysIleIleMetLysLysGluLysGluGluGly------IleGluLys 275
                                                                                                                                                                    ACATTTCCACGTCCAATGACAGATCGTGCAGGCCTTGATTTTAGTTTTTCTGGTTTAAAA
                                                                                                                                                                                                                                                                                                                                GGCGAAGCCTTTGATAAAACAGCAAAATTACTTGGACTA---GATTATCCA-----
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Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlp
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/Cgn2_1/USPTO_Epool_p/US10649273/runat_15062005_111416_6043/app_query.fasta_1.1429
-Q=/Cgn2_1/USPTO_Epool_p/US10649273/runat_15062005_111416_6043/app_query.fasta_1.1429
-DB=EST_-QFMT=fastap_-SUFFIX=p2n.rst_-MINMATCH=0.1 -LCOPCL=0 -LCOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRAMS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MILEN=-0 -MAXLEN=200000000
-USER=US10649273 @CGN 1 1 8076 @runat_15062005_111416_6043 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-NAMP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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ALIGNMENTS

JOURNAL MEDLINE PUBMED REFERENCE AUTHORS JOURNAL MEDLINE PUBMED REFERENCE REFERENCE AUTHORS TITLE SOURCE ORGANISM LOCUS DEFINITION RESULT 1 AK045669 ACCESSION VERSION KEYWORDS TITLE **AUTHORS** Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genome Res. 10 (10), 1617-1630 (2000) Meth. En 99279253 Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P. Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishi,Y., Nakamura,S., Hazama,M., Nishine,T., Haradda,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999) Bequence. AK045669 AK045669 2284 bp mRNA linear HTC 03-APR-200 Mus musculus adult male corpora quadrigemina cDNA, RIKEN full-length enriched library, clone:BE30219017 product:similar to PUTATIVE SIALOGLYCOPROTEASE TYPE 2 [Homo sapiens], full insert Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; Mus musculus Mus musculus (house mouse) AK045669.1 GI:26337528 11042159 Enzymol. Craniata; Vertebrata; Sciurognathi; Muridae; Muridae; Euteleostomi; HTC 03-APR-2004 genes

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Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Rike Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokoha Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Pax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Group Phase I & II Team:
Analysis of the mouse transcriptome
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 2284)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Functional annotation of a full-length mouse
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URL:http://fantom.gsc.riken.jp/.
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Please visit our web site for further details.
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/protein_id="BAC32450.1"
/db_xref="GI:6337529"
/translation="MuHARRITAGAIPKPPKSKVYGFLRRFSVHPRTLSCHKLVLGIET /translation="MuHARRITAGAIPKPPKSKVYGFLRRFSVHPRTLSCHKLVLGIET SCDDTGAAVVDETGNVLGEALHSQTQVHLKTGGIVPPVAQQLHRENIQRIVEETLSAC RITESDLSAIATTIKPGLALSLGVGLSPSLQLVNQFKKPFIPHHMBAHALSLIKHFECST RKGVFTSBFFLVLLISGGHCLLALVGVGLSFSLQLVNQFKKPFIPHHMBAHALSLIKHFECST VEFPFLVILISGGHCLLALVGVSSPFLLLGKNGSFFTSGDMLDKVARRLSLIKHFECST VEFPFLVILISGGHCLLALVGVSSPFLLLGKNGSFTSGDMLDKVARRLSLIKHFECST VEFPFLVILISGGHCLLALVGVSSPFLLLGKNGSFTSGDMLDKVARRLSLIKHFECST VEFPFLVILISGGHCLLALVGVSSPFLLGKNGSFTSGDMLDKVARRLSLIKHFECST VEFPFLVILISGGHCLLALVGVSSPFLLGKNGSFTSGDMLDKVARRLSLIKHFECST VEFPFLVILISGGHCLLALVGVSSPFLLGKNGSFTSGDMLDKVARRLSLIKHFECST VEFPFLVILISGGHCLLALVGVSSPFLLGKNGSFTSGDMLDKVARRLSLIKHFECST VEFFFLVILISGGHCLLALVGVSSPFLLGKNGSFTSGDMLDKVARRLSLIKHFECST VEFFFLVILISGGHCLLALVGVSSPFLLGKNGSFTSGDMLDKVARRLSLIKHFECST VEFFFLVILISGGHCLLALVGVSSPFLLGKNGSFTSGDMLDKVARRLSLIKHFECST VEFFFLVILISGGHCLLALVGVSSPFLLGKNGSFTSGDMLDKVARRLSLIKHFECST VEFFFLVILISGGHCLLALVGVSSPFLLGKNGSFTSGDMLDKVARRLSLIKHFECST VEFFFLXVARRLSLIKHFECST VEFFFLXVAR
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/mol_type="mRNA"
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/db_xref="taxon:10090"
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                                                                                                                                      Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kiteunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Pujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Ionue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AK011265 mRNA linear HTC 03-APR-2004 Mus musculus 10 days embryo whole body cDNA, RIKEN full-length enriched library, clone:2610001M19 product:similar to PUTATIVE SIALOGLYCOPROTEASE TYPE 2 [Homo sapiens], full insert sequence.
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Eukaryota; Metazoa;
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AK011265.1 GI:12847275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC) RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokoh Kanagawa 300-0045, Japan (B-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
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Analysis of the mouse transcriptome of 60,770 full-length cDNAs
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QILSSAADIAAAVQHATACHLAKRTHEAILFCKQKNLLSPANNVLVSGGVASNLYIR
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/clone_lib="RIKEN full-length
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Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Willalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Hellon, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
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USA

NIH-MGC Project URL: http://""-

Contact: MGC help desk

Email: cgapbs-rémail.nih.gov

Tissue Procurement: Marcello Bento Soares, Ph.D.

Tissue Procurement: Marcello Bento Soares, University of

""" Library Preparation: M. Bento Soares, University of

""" Library Preparation: M. Bento Soares, University of
                                                                                                                                                  Submitted (20-MAY-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                   Strausberg, R.
Direct Submission
                                                                                                                                                                                                                                                                                      human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (house
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mRNA (cDNA

400 1346 380 1286 360 1226 340

1406

Myers, R.M.,

Iowa

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US-10-649-273-2 (1-414) x BC030671 (1-1609)
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Best Local Similari
Query Match:
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 21312463
This clone has the following problem: frame shifted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clone distribution: MGC clone distribution information can be found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://www.systemsbiology.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA Sequencing by: Institute for Systems
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sValGluPheProPheLeuValLeuLeuIleSerGlyGlyHisCysLeuLeuAlaLeuVa
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                                                                                                                     sProPheIleProIleHisHisMetGluAlaHisAlaLeuThrIleArgLeuThrAsnLy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="Thymus gland, mouse"
/clone_lib="Soares_thymus_2NbMT"
/lab_host="DH108"
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/db_xref="taxon:10090"
/clone="IMAGE:1226118"
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                     1 (bases 1 to 870)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGENCOURT 7790948 NIH MGC 72 Homo 5', mRNA sequence
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                           http://image.llnl.gov
Plate: LLAM13342 row: 1 column:
                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                              Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BQ423651.1 GI:21118966
High quality sequence stop: 710.
                                                                  found through the I.M.A.G.E. Consortium/LLNL at:
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             PheTyrIleArgArgAlaLeuGluIleLeuThrAsnAlaThrGlnCysThrLeuLeuCys 350
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TTCTATATCCGCAGAGCTCTGGAAATTTTAACAAACGCAACACAGTGCACTTTGGTGTGT
                                                                    ArgAspLeuLeuProGlnAsnAsnAlaValLeuValAlaSerGlyGlyValAlaSerAsn
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/clone_lib="NIH MGC_72"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life
Technologies."
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/mol_type="mRNA"
/db_xref="taxon:9606"
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EX391919 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens
cDNA clone CSODKOO1YEO2 3-PRIME, mRNA sequence
EX391919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - France
Email: segref@genoscope.cns.fr Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mammalia; Eutheria; Primates; Catarrhini; Homin 1 (bases 1 to 852)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
On May 13, 2003 this sequence version replaced Contact: Genoscope
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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HisLeuLys---ThrGlyGlyIleValProProAlaAlaGlnGlnLeuHisArgGluAsn
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                                                                                                                                                                                                                                                                                           /cell type="HELA CELLS COT 25-NORMALIZED"
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/clone_lib="HOMO sapiens HELA CELLS COT 25-NORMALIZED"
/note="Ist strand cDNA was primed with a NotI-oligo(dT)
/note="Tist strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       clone="CS0DK001YE02"
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                                                                                                   2.41e-141
1353.50
96.14%
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AGENCOURT 8863711 NIH MGC 18
5', mRNA sequence.
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                                                                                         Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: DCTD/DTP/Gazdar
                                          Unpublished (1999)
                                                        NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
                                                                                                                                                                              BQ961028
BQ961028.1
                                                                                      Mammalia; Eutheria;
1 (bases 1 to 922)
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Homo sapiens cDNA clone
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MAGE:6423902
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US-10-649-273-2 (1-414) x BQ961028 (1-922)
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Query Match:
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CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLN
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information
found through the I.M.A.G.B. Consortium/LLNL at:
http://inage.llnl.gov
Plate: LLCM2603 row: d column: 15
                                                                                                                                                                                                                                                                                                                                                                                                                         LeuAlaLeuSerLeuGlyValGlyLeuSerPheSerLeuGlnLeuValGlyGlnLeuLys
SerAlaSerGlyValSerProSerAspLeuSerAlaIleAlaThrThrIleLysProGly
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                                                                                                                                                               MetLeuAspLysValAlaArgArgLeuSerLeuIleLysHisProGluCys-SerThrMe
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                                                                                        tSerGlyGlyLysAlaIleGluHisLeuAlaLysGlnGlyAsnArgPheHisPheAspIl
                                                                                                                                                                                                              GTTCAAGGAGTTTCAGATTTTCTGCTTCTTGGAAAGTCTTTGGACATAGCACCAGGTGAC
                                                                                                                                                                                                                                                                                  quality sequence stop: 584.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="IMAGE:6423902"
/tissue_type="large_cell_carcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 1B"
/clone_lib="NIH MGC 1B"
/clone_Torgan: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; CDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC_Library."
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/db_xref="taxon:9606"
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High quality sequence stop: 701.
Location/Qualifiers
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Tissue Procurement: DCTD/DTP
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National Institutes of Health, Mammalian
Unpublished (1999)
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
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Bovine Functional Genomics Laboratory
Animal and Natural Resources Institute
Bdlg. 200 Rm2A BARC-East, Beltsville, M
Tel: 3015048416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: tads@anri.barc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
0.00925 using options -trim_alt " -trim_fasta. Vector identified
by cross_match using options -minmatch 12 -minscore 18
plate: 45 row: M column: 02
Seg primer: CCCAGTCACGACGTTGTAAAACG
High quality sequence stop: 749.
Location/Qualifiers
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GAGGCTCATGCACTCACTATTAGGTTAACAAATAAGGTAGAATTTCCGTTTTTAGTTCTT
                                                                            GluAlaHisAlaLeuThrIleArgLeuThrAsnLysValGluPheProPheLeuValLeu
                                                                                                                        TCGTTTAGCTTACAACTGGTAGACCAGTTTAAAAAGCCCTTCATTCCCCATTCATCACATG
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                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="Pooled"
/tissue_type="Pooled"
/dev stage="Multiple"
/lab_host="DH10B T1 phage resistant"
/clone_lib="BARC 9BOV"
/note="Organ: Abomasum; Vector: pAgen-1; Site_1: EcoRV;
/site_2: Not1; Equimolar amounts of mRNA extracted from
fundic and pyloric abomasums of 18 and 21 week old steers.
Exposure to Ostertagia ostertagi was initiated at 15 weeks
of age. fundic and pyloric abomasum"
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/strain="Holstein"
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/clone="9BOV45_M02"
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                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 800)
Williams, D.R., Gracey, A.Y., Martin, S.L., Hughes, M.A., Li, W., Williams, D.R., Gracey, A.Y., Martin, S.L., Hughes, M.A., Li, W., Williams, D.R., Gracey, A.Y., Martin, S.L., Hughes, M.A., Li, W., Williams, D. and Cossins, A.R.
Roberts, For Expension Services Beautiful Contact: Andrew R. Cossins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Spermophilus lateralis (golden-mantled ground squirrel) Spermophilus lateralis
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CO738006.1 GI:50825276
EST.
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SlLH03c19e02f1 squirrel heart
clone 19e02 5', mRNA sequence
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Seq primer: pflc T7 (5'-AATACGACTCACTATAGGG-3')
High quality sequence stop: 800.
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                                                                                                                                                                                                                                                                                                                                     Email: cossins@liv.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Spermophilus.
                                                                                                                                                                                                                                                                                                                  Vector has been trimmed from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LysGluGluGlyIleGluLysGlyGlnIleLeuSerSerAlaAlaAspIleAlaAlaThr 288
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               /tissue_type="Heart"
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/lab_host="E.coli Electromax DH10B"
/clone_lib="squirrel heart library 1"
/clone_lib="squirrel heart library 1"
/note="Vector: pFLC; Site_1: Sall GTCGAG; Site_2: BamHI
/GGATCC; Normalized and subtracted cDNN library propared
                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                  /mol_type="mRNA"
/db_xref="taxon:76772"
                                                                                                                              sex="Male & female"
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1 (bases 1 to 1109)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
                                                                                                                                                         BM907988 1109 k
AGENCOURT 6707465 NIH MGC_119
5', mRNA sequence.
EM907988
                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                           Homo sapiens
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                                                                                                              Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies,
                                  ProPheIleProIleHisHisMetGluAlaHisAlaLeuThrIleArgLeuThrAsnLys 160
                                                                                                                                                                                                                                                                                   LeuGlyGluAlaIleHisSerGlnThrGluValHisLeuLysThrGlyGlyIleValPro
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                                                                                             AlaLeuSerLeuGlyValGlyLeuSerPheSerLeuGlnLeuValGlyGlnLeuLysLys 140
                                                                                                                                                           AlaSerGlyValSerProSerAspLeuSerAlaIleAlaThrThrIleLysProGlyLeu 120
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                   CCATTCATTCCCATTCATCATATGGAGGCTCATGCACTTACTATTAGGTTGACCAATAAA
                                                                                                                                           GCCAGTGGAGTCTCTCCAAGTGACCTCTCAGCAATTGCAACTACCATAAAACCAGGACTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone lib="NIH_MGC_119"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: EcoRV (destroyed); RNA source normal medulla from
anonymous male age 27. Library is oligo-dT primed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.3 kb, insert size range
o.9-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 013. Note:
this is a NIH_MGC Library."
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/mol_type="mRNA"
/db_xref="taxon:9606"
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/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CF114247 765 bp mRNA linear ES Shultzomica07498 Rat lung airway and parenchyma cDNA l Rattus norvegicus cDNA clone NA4935 5', mRNA sequence. CF114247
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Rattus norvegicus
Eukaryota, Metazoa, Chordata,
Mammalia, Eutheria, Rodentia,
                                                                                                                                                                                                                                   Average Phred score is 20 or better. All poor q 20) and vector/linker sequence has been removed High quality sequence stop: 765.
                                                                                                                                                                                                                                                                                                 Dept. of Molecular Biosciences, School of Veterinary Medicine University of California, Davis
1311 Haring Hall, One Shields Avenue, Davis, CA 95616, USA
Tel: 530 752 0793
Fax: 530 752 4698
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         /tissue_type="airway or parenchyma"
/dev stage="adult"
/clone_lib="Rat lung airway and parenchyma cDNA libraries"
/clone_lib="Rat lung; Vector: pGEM-11Zf(-); Site_1: Eco RI;
Site_2: Not I; mRNA was isolated from microdissected rat
lung airways and parenchyma tissues."
                                                                                                                            /clone="NA4935"
                                                                                                                                           /mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                             /sex="male"
                                                                                                                                                                                         organism="Rattus norvegicus"
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                               Homo sapiens cDNA clone
BQ636028
BQ636028.1 GI:21760487
EST.
                                                                                               BQ636028
hd03d11.y1 Human
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Touchman,J.W., Bouffard,G., Smith,D. and Peterson,K.
Expressed sequence tag analysis of human retina for the NEIBank
Project: Retbindin, an abundant, novel retinal cDNA and alternative
splicing of other retina-preferred gene transcripts
Mol. Vis. 8 (4), 196-204 (2002)
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National Eye Institute
6/331, NIH, Bethesda, MD
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1. (bases 1 to 640)
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Fax: 301 496 0078
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                      LysLysGluLysGluGluGlyIleGluLysGlyGlnIleLeuSerSerAlaAlaAspIle
                                                                                                  AlaLysAsnCysAspPheSerPheThrGlyLeuGlnHisValThrAspLysIleIleMet
                                                                              GCTAAAAATTGTGA
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[primer: M13RP1 reverse primer Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Organ: Eye; Vector: pSPORT1; Neural retina tissue was dissected from two 80 year old donors with no observe eye disease. 100ug of total RNA was used for library construction. A directionally cloned cDNA library in the pSPORT1 vector (Life Technologies) was constructed at Bisserve Biotechnology (Laurel MD) essentially following the protocols of the SuperScript Plasmid System full details of which are contained in the manufacturer's Instruction manual (http://www.lifetech.com/). First
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                primer-adapter [5'-pGACTAGTTCTAGATCGCGAGCGGCCGCCC(T)15-3']. EST and was performed on the unamplified library at the NIH Intramural Sequencing Center (NISC)."
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/db_xref="taxon:9606"
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/dev_stage="Adult"
/lab_host="EMDH10B"
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Veterihary Biomedical Sciences
University of Edinburgh
Summerhall Square, Edinburgh, EH9
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                                                                                                                                                                                                                                                                                              Seq primer: Ml3reverse High quality sequence s
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ovis aries
                                                                                                                                                                                                                                                                                                                            Email: j.hopkins@ed.ac.uk
Plate: 04 row: N column: 08
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Gossner, A. and Hopkins, J
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Mammalia; Eutheria;
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                                                                                                                                                             /clone="Oa_splbn_04N08"
/clone_lib="Sheep_spleen\brain
/note="Vector: pSport1"
                                                                                                                                                                                                        /organism="Ovis aries"
/mol_type="mRNA"
/db_xref="taxon:9940"
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CK833139.1
                             Construction and Analysis of a cDNA Library Intestinal Muscle and Epithelial Tissues of Unpublished (2004)
Contact: Richard G. Baumann
Ecvine Functional Genomics Lab
                                                                                                                               1 (bases 1 to 661)
Baumann,R.G., Baldwin,R.L., Sonstegard,T.S.,
Matukumalli,L.K.
                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                        Bos taurus
                                                                                                                                                                                                                                                                                                                                         4057170 BARC 8BOV
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                                                                                                                                                                                   Bovinae; Bos.
                                                                                                                                                                                                                                                         Bos taurus (cow)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LeuGlnHisValThrAspLysIleIleMetLysLysGluLysGluGluGlyIleGluLys
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 3015048604
                 162: BARC-EAST,
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Bos taurus
                                                                                                                                                                                                       Chordata; Craniata; Vertebrata; Euteleostomi; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
                   Beltsville,
                                                                                                                                                                                                                                                                                                                                           cDNA
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clone
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8BOV_20020 5', mRNA
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Best Local Similarity:
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Email: rbaumann@anri.barc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
0.00925 using options -trim_alt '' -trim_fasta. Vector identified
by cross match using options -minmatch 12 -minscore 18
plate: 20 row: O column: 20
plate: 20 row: O column: 20
seq primer: CCTATTRAGGTGACACTATAGGAAC
                                                                                                                    G1yLysSerLeuAspI1eAlaProG1yAspMetLeuAspLysValAlaArgArgLeuSer
                                                                                                                                                                                                                                                                           SerAlaIleAlaThrThrIleLysProGlyLeuAlaLeuSerLeuGlyValGlyLeuSer 129
                                                                                                                                                                                                                                                                                                                          ATATTCAACGCATAGTACAAGAAGCTCTCTCTGCCAGTGAAGTCTCTCCAAGTGAACTC
                                                                                                                                                                                                                                                                                                                                                                                                               GluValHisLeuLysThrGlyGlyIleValProProAlaAlaGlnGlnLeuHisArgGlu
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                                                                       IleSerGlyGlyHisCysLeuLeuAlaLeuValGlnGlyValSerAspPheLeuLeuLeu
                                                                                                                                                                                                          PheSerLeuGlnLeuValGlyGlnLeuLysLysProPheIleProIleHisHisMetGlu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="Epithelial, Muscle"
/dev stage="Lactating, Neonatal"
/lab_host="DH10B TonA"
/lab_host="DH10B TonA"
/clone_lib="BARC 8BOV"
/clone_Tib="BARC 8BOV"
/note="Torgan: Intestine; Vector: pCMVSport6.1; Site_1: EcoRI; Normalized cow cDNA intestinal—
NotI; Site_2: EcoRI; Normalized cow cDNA intestinal—
library in pCMVsport6.1, constructed from equimolar mRNA
pools derived from 5 sources, 4 lactating intestinal, 1
neonatal intestinal 4/5 Lactating, Proximal Duodenum,
Jejunum, Distal Ileum, Colon, 1/5 Neonatal, Proximal
Duodenum, Jejunum, Distal Ileum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="8BOV_20020"
/sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /strain="Holstein"
/db_xref="taxon:9913"
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|mol_type="mRNA"
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91.86%
48.87%
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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US-10-649-273-2 (1-414) x BQ43 Qy	Alignment Scores: 1.39e-1 Pred. No.: 1018.50 Score: 1018.50 Percent Similarity: 94.67% Best Local Similarity: 93.33% Query Match: 47.93% DB: 5	DAN Sequencing by: Agence Clone distribution: MGC or found through the I.M.A.G. http://image.llnl.gov Plate: LLAM13213 row: d Plate: LLAM13213 row: d Plate: LLAM13213 row: d Plate: LLAM13213 row: d Plate: LLAM13213 row: d Plate: LLAM13213 row: d Plate: LLAM13213 row: d Plate: LLAM13213 row: d Plate: LLAM13213 row: d Plate: LLAM13213 row: d Plate: LLAM13213 row: d Plate: LLAM13213 row: d Plate: LLAM13213 row: d Plate: LLAM13213 row: d Porganism="Homos s Porganism="Homos s Porganism="MAGE: 601 /Lione="MAGE: 601 /	Adminalia; Eutheria; Primates; C AUTHORS NIH-MGC http://mgc.nci.nih.gov/ TITLE National Institutes of Health, JOURNAL Unpublished (1999) COMMENT Contact: Robert Strausberg, Ph. Email: Cgapbs-remail.nih.gov Tissue Procurement: ATCC CDNA Library Preparation: Life	7760756 equence GI:211 15 (huma	Qy 250 Asp 250 	Db 479 GGGAAGTCTTTGGACA Qy 210 LeulleLysHisProc
1-414) x BQ433135 (1-879) LeuIleLeuThrLysThrAlaGlyValPhePheLysProSerLysArgLysValTyr 20	-103 Length: 879 50 Matches: 210 \$ Conservative: 3 \$ Mismatches: 9 \$ Indels: 3 Gaps: 1	DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be cund through the I.M.A.G.E. Consortium/LLNL at: ttp://image.llnl.gov late: LLAM13213 row: d column: 19 ligh qualify sequence stop: 674. Location/Qualifiers 1. 879 /organism="Homo sapiens" /mol type="mRNNA" /db_xref="taxon: 9606" /clone="IMAGE: 6016098" /tissue_type="embryonal carcinoma, cell line" /lab_host="DH10B (phage-resistant)" /clone lib="NHH_MCC_92" /note="Organ: testis; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: Sal1; Cloned unidirectionally; oligo-dT primed. Average insert size 2.5 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NHH_MGC_Library."	s; Catarrhini; Hominidae; Homo. gov/. th, Mammalian Gene Collection (M Ph.D. v	879 bp mRNA linear IIH_MGC_92 Homo sapiens cDNA clone 2211 Chordata; Craniata; Vertebrata; I		GGGAAGTCTTTGGACATAGCACCAGGTGACATGCTTGACAAGGTAGCAAGAAGACTTTCC 538 LeulleLysHisProGluCysSerThrMetSerGlyGlyLysAlaileGluHisLeuAla 229

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861 ATGGAANGGGT 871
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                                                                                                                                                           GlnGlyValSerAspPheLeuLeuLeuGlyLysSerLeuAspIleAlaProGlyAspMet 200
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                                    etSerGlyGly 222
                                                                                GCTTGACAAGGTGGGCAAGAAAGACTTTCTTTNATAANAACATTCCAAAGTGCTCCCCCC 860
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Search completed: June 17, 2005, 01:29:52 Job time: 3564.8 secs

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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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-UNITS=bits -START=1 -END=-1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST-45
-DCCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MAXIEN=-200000000
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-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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REFERENCE AUTHORS ACCESSION VERSION KEYWORDS RESULT 1 BQ423651 LOCUS FEATURES COMMENT SOURCE DEFINITION TITLE ORGANISM JOURNAL source CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium
CDNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1342 row: 1 column: 21
High quality sequence stop: 710. Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC/DCTD/DTP 1 (bases 1 to 870)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Homo sapiens BQ423651.1 GI:21118966 EST. BQ423651 870 bp AGENCOURT_7790948 NIH_MGC_72 Homo Unpublished (1999) Bukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; BQ423651 5', mRNA sequence. Homo sapiens (human) /mol_type="mRNA" /db_xref="taxon:9606" organism="Homo sapiens" Cocation/Qualifiers clone="IMAGE:6065828" .870 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo. sapiens cDNA clone mRNA linear EST 23-MAY-2002 e IMAGE:6065828

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Best Local Similarity:
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//lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC_72"
/clone_lib="NIH MGC_72"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
/site_2: SalI; Cloned unidirectionally. Primer: Oligo of the primer size 2 kb. Library constructed by Liftechnologies."
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Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokoham Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

Fax:81-45-503-9216)

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Rik
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Analysis of the mouse transcriptome based of 60,770 full_length CDNAs
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Location/Qualifiers
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Please visit our web site for further details.
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                    AsnCysAspPheSerPheThrGlyLeuGlnHisValThrAspLysIleIleMetLysLys
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AATTGCGATTTTTCTTTCACGGGACTTCAACATATTACTGATAAGCTAATAACACACAAG
                                                                       TTGGCCAAAGACGGAAATAGATTCCATTTTACTATCAATCCACCTATGCAGAATGCTAAG
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/cb_xref="01:26341pxppynlkxtgg1vpynqQilreniqriveetisac
RITPSDLSAIATTIKPGLALSIGVGLSFSLQLVNQFKKPFIPIHHMEAHALTIRLTNK
VEFPFLYILISGGHCILALVQGVSDFLLIGKSLDIARGOMLDKVARRLSIIKHPECST
MSGGKAIEQLAKDGNRFHFTINPPMQNAKNCDFSFTGLQHITDKLITHKEKEBGIEKG
MSGGKAIEQLAAVQHATACHLAKRTHRAILFCKQKNLLSPANAVILVVSGGVASNLYIR
KALEIVANATQCTLLCPPPRLCTDNGIMIAMNGIERLRAGLGVLHDVEDIRYEPKCPL
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                                  Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Suni, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Pujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsun, Inoue, Y., Tanaka, A. and Hayashizaki, Y. RIKEN integrated segmence analysis (RISA) system.—1394-format segmencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                         Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new Genome Res. 10 (10), 1617-1630 (2000)
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                    Genome Res.
20530913
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Kenic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome-gsc.riken.jp/, Tel:81-45-503-9222,
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
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Please visit our web site (http://genome.gsc.riken.jp/) for
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6 (bases 1 to 1622)
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/protein_id="bab27506.1"
/db_xref="GI:12847276"
/db_xref="GI:12847276"
/translation="mimilkrtagaipkppkskvygfilkrfsvhprtlschklvlgiet
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scddygaavudetgealhsgytoyhlkytggivppvagqlhrenigrivkltikltiklen
RITPSDLSAIATTIKPGLALSLGVGLSFSLQLVNQFKKPFIPIHHMEAHALTIRLTNK
VEFPFLVLLISGGHCLLALVQGVSDFLLGKSLDIAPGDMLDKVARRISLIKHPECST
MSGGKAIEQLAKDGNRFHFTINPPMQNAKNOTESTFGLOHITDKLITHKEEGGIEKE
GILSSAADIAAAVQHATACHLAKRTHRAILFCKQKNLLSPANAVLVVSGGVASNLYIR
RALEIVANATQCTLLCPPPRLCTDNGIMIAWNGIERLRAGLGVLHDVEDIRYEPKCPL
                                                                                                                                                                                                                                    /note="unnamed protein product; putative similar to PUTATIVE SIALOGLYCOPROTEASE TYPE 2 sapiens] (SPTR|Q9H4B0, evidence: FASTY, 80%ID,
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/strain="C57BL/6J"
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                          CCGCGATTAAAAATGGCACTT 1448
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Plate: 03 row: d column:
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                                                                              ArgArgLeuSerLeuIleLysHisProGluCysSerThrMetSerGlyGlyLysAlaIle
                     GluHisLeuAlaLysGlnGlyAsnArgPheHisPheAspIleLysProProLeuHisHis 98
GAACATTTGGCCAAACAAGGAAATAGATTTCATTTTGACATCAAACCTCCCTTGCATCAT 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 640)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 primer: M13RP1 reverse primer (ABI).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Organ: Eye; Vector: pSPORT1; Neural retina tissue was dissected from two 80 year old donors with no observed eye disease. 100ug of total RNA was used for library construction. A directionally clomed cDNA library in the pSPORT1 vector (Life Technologies) was constructed at Bioserve Biotechnology (Laurel MD) essentially following the protocols of the SuperScript Plasmid System full details of which are contained in the manufacturer's Instruction manual (http://www.lifetech.com/) First
                                                                                                                                                                                                                                                                                                                                                                                            Intramural Sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               strand synthesis was carried out using a Not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /dev_stage="Adult"
/lab_host="EMDH108"
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                                                                                                                                                                                                                                                                                                                                                                                                                 [5'-pGACTAGTTCTAGATCGCGAGCGGCCGCC(T)15-3']. EST analysis
was performed on the unamplified library at the NIH
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Conservative:
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alternative
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PEATURES

source

/mol_type="mRNA" /db_xref="taxon:9606" /organism="Homo sapiens"

'clone="CSODKOO1YEO2"

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ACCESSION
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KEYWORDS
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 852 bp mRNA linear BX391919 Homo sapiens HELA CELLS COT 25-NORWALIZED CDNA clone CSODKOO1YEO2 3-PRIME, mRNA sequence BX391919
                                                                                             2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr Ist strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                                                                      1 (bases 1 to 852)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 13, 2003 this sequence version replaced gi:30611736.
Contact: Genoscope
                                                                                                                                                                                                                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo
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                                      http://www.genoscope.cns.fr/cdna?s=CSOBAI035ZE07_CS03317_1&c=1240.
                                                         For more information about this cluster, see
                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (human)
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ORIGIN

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                                                                                                                DEFINITION
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Mus musculus
Mus musculus
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                                                                                            clone IMAGE:1226118),
                                                                                                                                                                                                    LeuLeuCysProProProArgLeu 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /cell_type="HELA CELLS COT 25-NORMALIZED"
/cell_line="HELA"
/clone_lib="Homo sapiens HRLA CTITE COM O
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                                                          GI:21040459
                                                                                                            O-sialoglycoprotein
                       (house mouse)
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                                                                                                                                1609 bp
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                                                                                             frame-shift errors.
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Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.L., Wang, J., Hsieh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Sthepleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalon, D.K., Muzny, D.M., Sodergren, B.J., Lu, X., Gibbs, R.A.,

Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,

Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,

Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, B.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,

Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Marcello Bento Soares, Ph.D.
Tissue Procurement: Marcello Bento Soares, University of Iowa
Library Preparation: M. Bento Soares, University of Iowa
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
thtp://www.systemsbiology.org
contact: amadan@systemsbiology.org
contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradh
Andan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortlum/LLNL at: http://image.llnl.gov Series: IRAK Plate: 66 Row: e Column: 10 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 21312463 This clone has the following problem: frame shifted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (20-MAY-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 1609)
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                                                                                                                                                                                                                                                                                                                                               /tissue type="Thymus gland, mous
/clone lib="Soares_thymus_2NbMT"
/lab_host="DH10B"
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/clone="IMAGE:1226118"
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                                                 Homo sapiens
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
I (bases i to 701)
                                                                                                                                                                                BE74061
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, h
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                           ProGlnLeuLysMetGluIle 267
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CCGCGATTAAAAATGGCACTT 139:
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                                                                                                                            sapiens (human)
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Email: cgapbs-r@mail.nih.gov

Tissue Procurement: DCTD/DTP

CDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can

found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plate: LLCM814 row: n column: 09
High quality sequence stop: 701.
Location/Qualifiers
 heCysLysGlnArgAspLeuLeuProGlnAsnAsnAlaValLeuValAlaSerGlyGlyV
                                                        laThrValGlnHisThrMetAlaCysHisLeuValLysArgThrHisArgAlaIleLeuP
                                                                                                                                                                                                                                                                                                                                                                  LeuSerLeuIleLysHisProGluCysSerThrMetSerGlyGlyLysAlaIleGluHis
                                                                                                                                                                                                                                                                                                                                                                                                                                       LeuLeuGlyLysSerLeuAspIleAlaProGlyAspMetLeuAspLysValAlaArgArg
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                                                                                                                              GGAAACAAGAGGAAGGTATTGAGAAGGGGCAAATCCTGTCTTCAGCAGCAGACATTGCTG
                                                                                                                                               ysGluLysGluGluGlyIleGluLysGlyGlnIleLeuSerSerAlaAlaAspIleAlaA
                                                                                                                                                                                                                      AsnCysAspPheSerPheThrGlyLeuGlnHisValThrAspLysIleIleMetLys--L
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                                                                                                                                                                                                       AATTGTGATTTTTCTTTTACTGGACTTCAACACGTTACTGATAAAATAATAATGAAAACA
                                                                                                                                                                                                                                                                             TTGGCCAAACAAGGAAATAGATTTCATTTTGACATCAAACCTCCCTTGCATCATGCTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="IMAGE:3949640"
/tissue_type="adenocarcinoma cell line"
/tissue_type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 9"
/clone_lib="NIH MGC 9"
/note="Organ: ovary; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; CDNA made by oligo-dT priming. DTectionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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1053.00
99.05%
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Matches:
Conservative:
Mismatches:
Indels:
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160

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Best Local Similarity:
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5', mRNA sequence
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Mammalia; Eutheria; Primates; Catarrhini;
1 (bases 1 to 922)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLCM2603 row: d column: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (human)
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLA
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alAlaSerAsnPheTyrIleArgArgAlaLeuGluIleLeuThrAsnAlaThrGlnCysT
              LeuLeulleSerGlyGlyHisCysLeuLeuAlaLeuValGlnGlyValSerAspPheLeu 40
                                                                           MetGluAlaHisAlaLeuThrIleArgLeuThrAsnLysValGluPheProPheLeuVal
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                                                                                                                   _COPY_148_414 (1-267)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             quality sequence stop: 584.
Location/Qualifiers
                                                                                                                                                                                                                                                                                    /tissue_type="large cell carcinoma"
/lab host="DHIOB (phage-resistant)"
/clone_lib="NIH_MGC_18"
/clone_lib="NIH_MGC_18"
/clone="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI, Site 2:
/corI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of: California,
Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Homo sapiens"
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0829596 MARC 3PIG Sus scrofa cDNA 3'

07362328

07362328.1 GI:34161882

EST.

Sus scrofa (pig)
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                                                                     cross match v0.990329.
Plate: SRG8015 row: H column:
Seq primer: TAGAAGGCACAGTCGAGG.
                                                                                                                                                                                  USDA, ARS, US Meat Animal
PO Box 166, Clay Center, h
Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                   Unpublished (2003)
Contact: Smith TPL
                                                                                                                                                                                                                                                                                                          Smith, T.P.L., Freking, B.A., Ford, J.J., Vallet, J.L., Fox, J., Wise, T.A., Nonneman, D.J., Wray, J.E. and Keele, J.W. A second set of porcine ESTs from a pooled-tissue normalize
                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 658)
                                                                                                                           Single pass sequencing. Bases called trimmed with the aid of the trim_alt
                                                                                                                                                                  Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                           library
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/organism="Sus scrofa"
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                                                         Location/Qualifiers
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                                     Galius galius
                                                 Gallus gallus (chicken)
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/tissue_type="pooled"
/lab host="DH10B"
/clone_lib="MARC 3PIG"
/clone_lib="MARC 3PIG"
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Library made with RNA pooled #rom multiple tissues
including brain, liver, muscle, placenta/endometrium,
ovary, testes, and bone marrow."
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Wittzell,H., Bed'Hom,B., Morin,V., )
Chausse,A.M. and Zoorob,R.
A collection of chicken ESTs from ac
Unpublished (2003)
Contact: Zoorob R
UPR 1983
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Tel: 33 1 49 58 35 00
Fax: 33 1 49 58 33 81
Email: zoorob@vjf.cnrs.fr.
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|CAAGTAATCAGTATATCAGAAAAGGACTGCAGACTCTGGCAAATGCAAACGGTTTTGCT
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LeuLeuCysProProProArgLeuCysThrAspAsnGlyIleMetIleAlaTrpAsnGly
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/db_xref="taxon:9031"
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Sonstegard, T.S., Van Tassell, C.P., Matukumalli, L.K., Harhay, G.P., Bosak, S., Rubenfield, M. and Gasbarre, L.C.
Production of EST from cDNA libraries derived from immunologically activated bovine gut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Povinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: tads@anri.barc.usda.gov
Single pass sequencing. Bases called and trimmed with p
0.00925 using options -trim_alt "-trim_fasta. Vector
by cross match using options -minmatch 12 -minscore 18
plate: 12 row: F column: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Tad S. Sonstegard
Bovine Functional Genomics Laboratory
Animal and Natural Resources Institute
Bdlg. 200 Rm2A BARC-East, Beltsville, N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2004)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3015048416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    quality sequence stop: 637.
                                                                                                                                     /dev_stage="Multiple"
/lab host="pHHUB Ti phage resistant"
/lab host="pHHUB Ti phage resistant"
/clone_lib="BARC 10BOV"
/note="Organ: Small Intestine; Vector: pAgen-1; Site 1:
/note="Organ: Small Intestine; Vector: pAgen-1; Site 1:
ECORV; Site_2: NotI; Equimolar amounts of mRNA extracted
from proximal jejunums of 18 and 21 wk old steers, and
distal ileums of 14 day old calves. proximal jejunum
exposed to C. oncophora for 3 and 6 weeks, and distal
ileum exposed to C. parvum for 7 days"
                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:9913"
/clone="10BOV12_F24"
                                                                                                                                                                                                                                                                                                                                                                                           organism="Bos taurus"
mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                            sex="Male"
                                                                                                                                                                                                                                                                                                                                                                              strain="Holstein"
                                                                                                                                                                                                                                                                                                       tissue_type="Pooled"
 5.09e-8
838.00
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92 AGATTAAAAATGAAGATT
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                                                                                                                                                                                              McCarrey,J., Eddy,M., Marra,M., Hillier,L., Clifton,S., Martin,J., Wylie,T., Dante,M., Bowers,Y., Theising,B., Ritter,E., Tsaggareishvili,R., Ronko,I., Maguire,L., Ke. Bennett,J., Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                 CB272391 597 bp mRNA linear EST 24-FEB-: mai57g12.y1 McCarrey Eddy spermatocytes Mus musculus cDNA clone IMAGE:6445750 5' similar to TR:Q9VWD6 Q9VWD6 CG14231 PROTEIN.;
Email: est@watson.wustl.edu
Library constructed and donated by
Foundation for Biomedical Research,
                                                                      4444 Forest Park Parkway, Tel: 314 286 1800
                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                mRNA sequence.
CB272391
                                                                                                             Washington University
                                                                                                                                            Contact: McCarrey/Eddy NIEHS Mouse
                                                                                                                                                             Unpublished (2002)
                                                                                                                                                                                                                                                                    Mammalia; Eutheria;
1 (bases 1 to 597)
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                                                   Fax: 314 286 1810
                                                                                                                             NIEHS Mouse
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                                                                                      School of Medicine way, Box 8501, St. )
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                                                                                                                                                                                                                                                                                     Craniata; Vertebrata;
Sciurognathi; Muridae
 by J. McCarrey, Ph.D.
rch, Dept. of Genetics)
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Clifton, S., Muridae;

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Institute
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AsnCysAspPheSerPheThrGlyLeuGlnHisValThrAspLysIleIleMetLysLys 120
                                                                                                              TTGGCCAAAGACGGAAATAGATTCCATTTTACTATCAATCCACCTATGCAGAATGCTAAG
                                                                                                                                     LeuAlaLysGlnGlyAsnArgPheHisPheAspIleLysProProLeuHisHisAlaLys 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="spermatocytes, pooled
/dev_stage="60 day"
/lab_host="DH10B (phage-resistant)"
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Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., E
Boardman, P.E., Sanz-Ezquerro, J., Wilson, S.A.
Pong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A.
A Comprehensive Collection of Chicken cDNAs
Corr. Biol. 12 (22), 1965-1969 (2002)
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EST.
Gallus gallus (chicken)
Gallus gallus
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
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/clone lib="CSEQCHN59"
/clone ib="CSEQCHN59"
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/lab_host="DH10B"
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TITION Oa_splbn_04N08_M13reverse Sheep spleen\brain pSport1 library Ovis aries cDNA clone Oa_splbn_04N08 5', mRNA sequence.

ION CN823245

N CN823245.1 GI:47951314

DS Ovis aries (sheep)

Ovis aries
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Caprinae; Ovis.
1 (bases 1 to 730)
RS Gossner,A. and Hopkins,J.
Ovine spleen\brain cDNA library
Contact: J Hopkins
Contact: J Hopkins
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High quality sequence
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                                                                                                                                            CysLysGlnArgAspLeuLeuProGlnAsnAsnAlaValLeuValAlaSerGlyGly
                                                                                                                               TGCAAGCAGAGAGGCTTGTTACATCAAAGTAACGCAGTACTGGTTGTATCTGGAGGC
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Location/Qualifiers
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/clone lib="Sheep spleen\brain ps/
/note="Vector: pSport1"
                                                               545 bp
Bos taurus kidney fetus
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                                      ThrValGlnHisThrMetAlaCysHisLeuValLysArgThrHisArgAlaIleLeuPhe 160
                                                                                                                                                    GluLysGluGluGlyIleGluLysGlyGlnIleLeuSerSerAlaAlaAspIleAlaAla 140
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GCAGTCCAGCACACCGTAGCCTGCCACGTTGCNAAAAGAACACATCGCGCTATTCTGTTC
                                                                                                                     GAAAAAGGAAGGTATCGAGCAGGGGCAGATCCTGTCTCAGCTGCAGACATTGCTGCT
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Best Local Similarity:
Query Match:
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Establishment of a high throughput EST sequencing system using poly(A) tail-removed cDNA libraries and determination of 36,000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Single pass sequencing.
This clone was obtained from a polyA-deleted cDNA library.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shirakawa Institute of Animal Genetics
Odakura, Nishigo, Nishi-shirakawa, Fuku
Tel: 81-248-25-5641
Fax: 81-248-25-5725
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21570554
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Yoshikazu Sugimo
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                                                                                                                                                                                                                                                                                            eSerPheThrGlyLeuGlnHisValThrAspLysIleIleMetLysLysGluLysGluLj 124
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oProProArgLeuCysThrAspAsnGlyIleMetIleAlaTrpAsnGlyIleGluArgLe
                                                        GASPLeuLeuProGlnAsnAsnAlavalLeuValAlaSerGlyGlyValAlaSerAsnPh 184
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was deleted from a Not1 site"
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Search completed: June 17, 2005, 01:30:00 Job time: 2296.07 secs

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Scoring table:
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-Q-/Cgn2 1/USPTO_spool_p/US10649273/runat_15062005_111416_6043/app_query.fasta_1.1429
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-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
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-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
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-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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                                                            Tissue Procureway.

CDNA Library Preparation: Life Technology CDNA Library Preparation: Life Technology CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL) CDNA Library Arrayed by: The I.M.A.G.B. Consortium DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at: http://image.llnl.gov http://image.llnl.gov l column: 21
Plate: LLAMI3342 row: 1 column: 21
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                      5', mRNA sequence.
BQ423651
                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                           BQ423651 870 bp mRNA linear EST 23-MAY-200:
AGENCOURT 7790948 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6065828
                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                         Homo sapiens
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                                                                                                                                                                                                                              Mammalian
                                                                                                                                                                                                                               Gene Collection (MGC)
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CD508917 BX359023

BU246158

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UI-R-CA1-BX359023 CDA93-E05 BX776940

CR444994 BQ672554

CR444994 AJ647827

AGENCOURT 603491570

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EST 23-MAY-2002

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603739448 UI-H-FL1ssalrgb54

BovGen_09 BB043703

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604138456 RC1-BT025

BU261251 CK365185

603502215 AGENCOURT

BU621780

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UI-CF-FN0 AV602901 AGENCOURT

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RESULT 2
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              BQ636028 640 bp mRNA linear EST 15-hd03d11.y1 Human Retina cDNA (Un-normalized, unamplified): Homo sapiens cDNA clone hd03d11 5', mRNA sequence.
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 72"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
/site_2: SalI; Cloned unidirectionally. Primer: Oligo of Average insert size 2 kb. Library constructed by Lift Technologies."
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1 (bases 1 to 640)

Wistow,G., Bernstein,S.L., Wyatt,M.K., Ray,S., Behal,A.,
Touchman,J.W., Bouffard,G., Smith,D. and Peterson,K.

Expressed sequence tag analysis of human retina for the NEIBank
Project: Retbindin, an abundant, novel retinal cDNA and alternative points of the retinal cDNA and alternative points of the retinal cDNA and alternative points.
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National Eye Institute
6/331, NIH, Bethesda, MD 20892-2740, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: graeme@helix.nih.
Plate: 03 row: d colum
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Fax: 301 496 0078
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                    AlaLysAsnCysAspPheSerPheThrGlyLeuGlnHisValThrAspLysIleIleMet 90
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GCTAAAAATTGTGATTTTTTTTTTACTGGACTTCAACACGTTACTGATAAAATAATAATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Organ: Eye; Vector: pSPORT1; Neural retina tissue was dissected from two 80 year old donors with no observed eye disease. 100ug of total RNA was used for library construction. A directionally cloned cDNA library in the pSPORT1 vector (Life Technologies) was constructed at Bioserve Biotechnology (Laurel MD) essentially following the protocols of the SuperScript. Plasmid System full details of which are contained in the manufacturer's Instruction manual (http://www.lifetech.com/). First
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          strand synthesis was carried out using a Not
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unamplified): hd/he"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [5'-pGACTAGTTCTAGATCGCGAGCGGCCCCC(T)15-3']. EST an-
was performed on the unamplified library at the NIH
Intramural Sequencing Center (NISC)."
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/dev_stage="Adult"
/lab_host="EMDH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="hd03d11"
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Hirozane, T.,

Carninci, P.,

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2284 bp mRNA linear nic vo conduction musculus adult male corpora quadrigemina cDNA, RIKEN full-length enriched library, clone:B230219017 product:similar to comparative ctarographycoprotease Type 2 [Homo sapiens], full insert
                                          Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishi, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Pujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                            Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                        Genome Res.
20530913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning
Meth_Enzymol. 303, 19-44 (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (B-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
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Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraka, T., Kinoza
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Analysis of the mouse transcriptome of 60,770 full-length CDNAs
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The RIKEN Genome Exploration Research Group Phase
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Please visit our web site for further details.
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URL:http://fantom.gsc.riken.jp/
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//ProteIn_id="BAC32450.1"
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//COGOTGAAVVDETGNVLGEALHSQTQVHLKTGGIVPPVAQQLHRENIQRIVEETLSAC
RITPSDLSAIATTIKFGLALSLGVGLSFSLQLVNQFKKPFIPIHHMEAHALTIRLTNK
VEFPFLVLLISGGHCLHALVQGVSDFLLLGKSLDIAFGDMLDKVARRESLIKHPECST
MSGGKAIEQLAXDGNRFHFTINPFMQNAKNCDFSFTGLQHITDKLITHKEKEEGIEKG
QILSSAADIAAAVQHATACHLAKRTHRAILFCKQKNLLSPANAVLVVSGGVASNLYIR
KALEIVANATQCTLLCPPPRLCTDNGINIAMNGIERLRAGLGVLHDVEDIRYEPKCPL
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                                                                                                                            GVDISREVABAAIKVPRLKMAL"
                                                      /note="putative"
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                                                                                                                                                          AK011265 1622 bp mRNA linear HTC 03-APR-2004 Mus musculus 10 days embryo whole body cDNA, RIKEN full-length enriched library, clone:2610001M19 product:similar to PUTATIVE SIALOGLYCOPROTEASE TYPE 2 [Homo sapiens], full insert sequence.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                              Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
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Analysis of the mouse transcriptome based of 60,770 full-length cDNAs
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High-efficiency full-length cDNA cloning
Meth Enzymol. 303, 19-44 (1999)
                                                                                                                                                                                                                                      cDNA library was prepared and sequenced
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                                                                                                                                                                                                                                                                             web site (http://genome.gsc.riken.jp/) for further
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MSGGKAIEQLAKDGNRFHFTINPPMQNAKNCDFSFTGLQHITDKLITHKEKEEGIEKE
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/clone_Tib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="10 days embryo"
207 - 1/67
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
On May 13, 2003 this sequence version replaced gi:30611736.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr lst strand cDNA was primed with a NotI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSDDK001YE02"
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                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. CE 1 (bases 1 to 1609)

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diacchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Schmerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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Strausberg, R.
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 21312463
This clone has the following problem: frame shifted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Marcello Bento Soares, Ph.D.
cDNA Library Preparation: M. Bento Soares, University of
cDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://www.systemsbiology.org
contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clone distribution: MGC clone distribution
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                          HisLeuValLysArgThrHisArgAlaIleLeuPheCysLysGlnArgAspLeuLeuPro 140
                                                                                                                                       GlyGlnIleLeuSerSerAlaAlaAspIleAlaAlaThrValGlnHisThrMetAlaCys 120
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CACCTTGCGAAAAGAACACATCGCGCTATTCTGTTTTGCAAGCAGAAAAATTTGCTCTCT 1168
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/clone lib="Soares_thymus_2NbMT"
/lab_host="DH10B"
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/mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov Plate: LLCM814 row: n column: 09
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Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
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National Institutes of Health, Mammalian
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1 (bases 1 to 701)
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/tissue_type="adenocarcinoma cell line"
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98.91%
97.27%
73.23%
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                    Contact: Smith TPL
USDA, ARS, US Meat Animal R
PO Box 166, Clay Center, NE
Tel: 402 762 4366
Fax: 402 762 4390
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                                            Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with trimmed with the aid of the trim_alt optio
cross_match_v0.990129.
Plate: SRG8015 row: H column: 12
Seq primer: TAGAAGGCACAGTCGAGG.
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Smith, T.P.L., Freking, B.A., Ford, J.J., Vallet, J.L., Wise, T.A., Nonneman, D.J., Wray, J.E. and Keele, J.W.
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
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/lab_host="DH10B"
/clone_lib="MARC 3PIG"
/note="Vector: pcDNA3.:
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/mol_type="mRNA"
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Single pass sequencing. Bases called
0.000925 using options -trim_alt "-
by cross match using options -minmat
plate: 12 row: F column: 24
Seq primer: AGCGGATAACAATTCACACAGG
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Bovine Functional Genomics Laboratory
Animal and Natural Resources Institute
Bdlg. 200 Rm2A BARC-East, Beltsville, MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 activated bovine gut
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Sonstegard, T.S., Van Tassell, C.P., Matukumalli, G.P., Bosak, S., Rubenfield, M. and Gasbarre, L.C. Production of EST from cDNA libraries derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fax: 3015048414
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SerAsnPheTyrIleArgArgAlaLeuGluIleLeuThrAsnAlaThrGlnCysThrLeu
                                                                                                                                                                                                                                                                                                                                                                                                                        ValGlnHisThrMetAlaCysHisLeuValLysArgThrHisArgAlaIleLeuPheCys 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LysGluGluGlyIleGluLysGlyGlnIleLeuSerSerAlaAlaAspIleAlaAlaThr 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CysAspPheSerPheThrGlyLeuGlnHisValThrAspLysIleIleMetLysLysGlu 93
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                                                                                                                                                                                                                      LysGlnArgAspLeuLeuProGlnAsnAsnAlaValLeuValAlaSerGlyGlyValAla 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGTGATTTTTCTTTTTCTGGACTTCAACACGTTATTGATAAGATGATAATGCAAAAGGAA
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                                                                                                                                                          AAGCAGAGAGGCTTCTTACGTCAGAGTAACGCAGTACTGGTTGTATCTGGAGGCGTCGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANAGAGGAAGGTATCGAGCAGGGGCAGGTCCTGTCTTCAGCTGCAGACATTGCTGTTGCG
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Location/Qualifiers
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/lab host="DHIOB TI phage resistant"
/clone_lib="BARC 10BOV"
/note="Organ: Small Intestine; Vector: pagen-1; Site_1:
/note="Organ: Small Intestine; Vector: pagen-1; Site_1:
/note="Organ: Small Intestine; Vector: pagen-1; Site_1:
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/db_xref="taxon:9913"
/clone="10BOV12_F24"
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/mol_type="mRNA"
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US-10-649-273-2_COPY_176_414 (1-239)
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1 (bases 1 to 922)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
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AGENCOURT 8863711 NIH MGC 18
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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                                                                                                                                                                                                                                      /clone="IMAGE:6423902"
/tlosue_type="large_cell_carcinoma"
/tlab_host="DH10B (phage-resistant)"
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/clone_lib="NIH MGC_18"
/clone_lib="NIH MGC_18"
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AV602901
3', mRNA
                          Contact: Yoshikazu Sugimoto
Animal Genetics Division
Shirakawa Institute of Animal Genetics
Odakura, Nishigo, Nishi-shirakawa, Puk
Tel: 81-248-25-5641
                                                                                                                                                                                                                      Establishment of a high throughput EST sequencing poly(A) tail-removed cDNA libraries and determinate
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and Sugimoto,Y.
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    CATTATTGATGGCTGGGGAAGGGAATTGAAAAAAATA

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CB852881 490 bp mRNA linear EST 22-A: UI-CF-FNO-afo-b-03-0-UI.sl UI-CF-FNO Homo sapiens cDNA clone UI-CF-FNO-afo-b-03-0-UI 3', mRNA sequence.
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clone was obtained from a polyA-deleted cDNA library
Location/Qualifiers
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/clone="B1KI013A07"
/tissue_type="kidney"
/dev_stage="fetus"
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/note="Vector: pZL1; Site_1: Sal1; Site_2: Not1; Poly
was deleted from a Not1 site"
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/mol_type="mRNA"
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Tissue Procurement: Dr. M. J. Welsh, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com) or from Open Biosystems
(www.openbiosystems.com).
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Tel: 319 356 4866
Fax: 319 356 7171
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McCray Lab
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/tissue type="Human Lung Epithelial cells"
/lab host="PHHOB (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-CF-FNO"
/note="Organ: Lung; Vector: pT773-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I;
UI-CF-FNO is a subtracted CDNA library derived from two normalized Human lung epithelial cell libraries (EN1 and DU1) The library was subtracted according to according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. For additional information, contact:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        bento-soares@uiowa.edu
TAG_SEQ=None found"
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/db_xref="taxon:9606"
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1 (bases 1 to 822)
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Gallus gallus
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 33 1 49 58 35 00 Fax: 33 1 49 58 33 81
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                                         IleArgTyrGluProLysCysPro 216
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CysSerThrMetSerGlyGlyLysAlaIleGluHisLeuAlaLysGlnGlyAsnArgPhe
                                                                                                                                                                                                                                                                                                                                                                                                                          zoorob@vjf.cnrs.fr.
                                                                                                                                                                                                                                                                                                           /organism="Gallus gallus"
/mol type="mRNA"
/db xref="taxon:9031"
/cell type="Splenocytes"
/clone lib="PHA-activated s
/note="Vector: pTriplEX2"
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                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves; Neognathae; Galliformes; Phasiani Phasianinae; Gallus.
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Gallus gallus
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603114407F1 CSEQCHL20 Gallus
                                                                                                                                                                                    Contact: Simon Hubbard
Department of Biomolecular Sciences
                                                                                                                              PO Box 88, Manchester, Tel: 01612008930
                                                                                                                                                                       Department of Biomolecular Sciences
University of Manchester Institute of Science
                                                                                                                  Pax: 01612360409
                                                                                                                                                            (UMIST)
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                                                                                                                                                                                                                                                                                                 (bases 1 to 866)
                                                                                                  Simon. Hubbard@umist.ac.uk
                 /mol type="mRNA"
/strain="White Leghorn, Hisex"
/db_xref="taxon:9031"
                                                                                    ocation/Qualifiers
     clone="ChEST66m2"
                                                          organism-"Gallus gallus"
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IleSerLysGluValGlyGluAlaSerIleLysValProGlnLeuLys 236
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                                                                                                                                                                                                                                                             AlaLeuGluIleLeuThrAsnAlaThrGlnCysThrLeuLeuCysProProProArgLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LeuGlnHisValThrAspLysIleIleMetLysLysGluLysGluGluGlyIleGluLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CysSerThrMetSerGlyGlyLysAlaIleGluHisLeuAlaLysGlnGlyAsnArgPhe
                                                                                                                                       TGCACCGATAATGGTGTTATGATTGCATGGAATGGCATTGAAAGGTTGCGTGCAGGATGT
                                                                                                                                                                                                                     GGACTGCAGACTCTGGC-AATGCAAACGGTTTTGCTTTTCTGTCTCCTCCTCCAAGGCTG
                                                                                                                                                                                                                                                                                                      CCAAAAACTGCAACTCTGGTTGTATCAGGAGGAGTTGCAAGTAATCAGTATATCAGAAAA
                                                                                                                                                                                                                                                                                                                                                                                      CATATTATCCAGCGGACACACCGAGCCATGCTCTTCTGCATGAAAAAACAGCATATTATTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGGGAAATCCTGTCCTGCGTTAAGGACATCGCTGCTGCTGCACAGCATGTAGTGGCTGCT
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/lab_host="DH108"
/clone_lib="CSEQCHL20"
/clone_lib="CSEQCHL20"
/note="Organ: limbs; Vector: pBluescript II KS(+); Site 1:
ECORI; Site 2: Not1; Modification of pBluescript II KS(+)
[Stratagene] vector to accommodate cDNA produced with the
T-trimmed protocol (Construction of uni_directionally
cloned cDNA libraries from messenger RNA for improved 3'
end DNA sequencing by Glenn Fu, et al. U.S. Patent #
6,387,624). Cut pBluescript II KS(+) with NotI and EcoRI.
Ligate in double stranded adaptor containing BsgI and
BamHI sites [5'ggccgcgtgcaggctgcagg]
[5'aattcttttttcggatccggggctgcacgc]"
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Matches:
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                 Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                               Score:
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113 ThrValGlnHisThrMetAlaCysHisLeuValLysArgThrHisArgAlaIleLeuPhe 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-remail.nih.gov
Tissue Procurement: Howard Jacobs
cDNA Library Preparation: Express Genomics
cDNA Library Preparation: Express Genomics
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM14944 row: d column: 02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             High quality sequence stop: 736.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
Unpublished (1999)
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736 bp mRNA linear EST 23-I
AGENCOURT 17157291 NIH MGC 231 Rattus norvegicus cDNA clone
IMAGE:7097620 5', mRNA sequence.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Norway
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                                                                           GluLysGluGluGlyIleGluLysGlyGlnIleLeuSerSerAlaAlaAspIleAlaAla 112
                                                                                                                                                                                 AsnCysAspPheSerPheThrGlyLeuGlnHisValThrAspLysIleIleMetLysLys
                                                                                                                                                       AACTGTGATTTTTCTTTTACGGGACTTCAACATGTCACCGATAAGCTAATAACACACAAG
                                                    GAAAAAGAAGAAGGCATTGAGAAGGGGCAAATCCTGTCATCAGCCGCAGACATTGCTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              bases 1 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone lib="NIH MGC_231"
/clone | lib="NIH MGC_231"
/note="Organ: lung; Vector: pExpress-1; Site_1: EcoRV;
/note="Organ: lung; Vector: from pooled lung tissue from a
Site_2: NotI; RNA obtained from pooled lung tissue were
snap frozen and female animals at 8 wk old. Tissues were
snap-frozen and kept at -80C for two days before RNA
extraction and purification (Tri-reagent method). cDNA was
primed using oligo-dT primer:
5'-pGACTAGTTCTAGATCGCGAGCGGCCC(T)25-3' and cloned into
the EcoRV/NotI sites of pExpress-1. Size-selection >1.4kb
resulted in an average insert size of 2.3 kb. This primary
library is not normalized (normalized primary library is
NIH MGC_232) and was constructed by Express Genomics
(Prederick, MD). Note: this is a NIH_MGC library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tissue_type="lung, pooled"
lab_host="DH10B TonA"
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	Search completed: June 17, 2005, 01:30:06 Job time : 2054.13 secs	Search completed: June Job time : 2054.13 secs	Jo. Se
	CCACGATTAAAAATGACACTT 501	481	дb
	ProGlnLeuLysMetGluIle 239	233	S
480	CCAAAATGTCCTCTCGGAATAGACATATCCAGAGAAGTTGCAGAAGCTGCCATAAAAGTA	421	밁
232	GluValGlyGluAlaSerIleLysVal	213	S
420	ATTGAAAGATTACGTGCTTGGGCATTTTACATGATGTAGAAGACATCCGATACGAA	361	뮍
212	IleGluArgLeuArgAlaGlyLeuGlyIleLeuHisAspIleGluGlyIleArgTyrGlu	193	S
360	TTGTTGTGTCCCCCTCCGAGACTGTGCACTGACAATGGTATCATGATTGCATGGAATGGA 360	301	망
192	LeuLeuCysProProProArgLeuCysThrAspAsnGlyIleMetIleAlaTrpAsnGly	173	Ş
300	GCAAGTAACTTGTACATCCGAAGAGCATTGGAAATTGTAGCAAATGCAACACAATGCACT 300	241	망
172	AlaSerAsnPheTyrIleArgArgAlaLeuGluIleLeuThrAsnAlaThrGlnCysThr	153	δ.
240	TGCCAGCAGAAAAATTTGCTATCTCCAGCTAACGCAGTATTAGTTGTGTCTGGAGGTGTT	181	밁
152	InArgAspLeuLeuProGlnAsnAsnAlaValLeuValAlaSerGlyGlyVal	133	Ş
180		121	Дb